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29-MAR-2000; 2000WO-EP02769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGCTTTCAAGATACAGCTCGACACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTAC
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                                                                                                                                   plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance activity
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; Pred. No. 0;
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                                             Reed JN,
NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                                                                                                                                             8; Page 48-49; 62pp; English.
                                             Salmeron JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%;
Matches 1356; Conservative 0
                                                                                          2000-679374/66.
                                             Peters C,
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                                                                  ATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCATCAACAAGGTTCGTGTCG
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/product= Trichothecene resistance polypeptide
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                                                                                                                                                       Trichothecin 3-0-acetyltransferase gene useful as a selective marker in gene manipulations in eukaryotic host cells -
                                                                                                                                                                                                                              This invention describes a novel protein with trichothecin 3-0-acetyltransferase activity. The gene is used as a selective marker in a gene manipulation using eukaryote as the host cell. This sequence encodes the trichothecin 3-0-acetyltransferase isolated from Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCCAAATCAGTCTCTCTACCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGC
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                                                                                                                                                                                                                                                                                                                                                             Score 1340; DB
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                    Claim 3; Page 16-18; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                             98.8%;
98JP-0200280
                                98JP-0200280
                                                            (RIKA ) RIKAGAKU KENKYUSHO.
(YAMA/) YAMAGUCHI I.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                         2000-274037/24.
                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                        P-PSDB; AAY51848
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                              15-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                          Matches 1346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCGAGCAAGGTCTTAAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAAGGTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                           Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichotheceme resistance
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                                                                                                                                                                                Dawson JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1403 BP; 350 A; 397 C; 352 G; 304 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 915.6; DB 21;
Pred. No. 6.2e-281;
0; Mismatches 264;
                                                                                                                                                                                Reed JN,
                                                                                                                                      MBH
                                                                                                                                      GES
                                                                                                                                                                                  Salmeron JM,
                                                                                                                                      VERW
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 46; 62pp; English.
                                                                                                              (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN
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                                       99US-0282995
2000US-0502852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.3 Matches 1087; Conservative
                                                                                                                                                                                                                              2000-679374/66
                                                                                                                                                                                  Peters C,
                                                                                                                                                                                                                                 WPI; 2000-679374,
P-PSDB; AAB03934
                                         31-MAR-1999;
11-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trichothecene resistance can be used to transform plant cells to make them resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Pusarium that produces a trichothecene, preferably comprising a C.3 hydroxyl group, by growing transformed crop plants in an area which comprises the Zea mays ubiquitin promoter, the phosphate mannose isomorase selectable marker and the nopaline synthase termination sequence. PNOV1704 further comprises the Zea mays ubiduiting promoter, the phosphate mannose termination sequence. PNOV1704 further comprises the Zea mays ubiduitin promoter operably linked to the trichothecene 3-O-acetyl transferases sequence given in GENESEQ record AAA54206 and the nos
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Pred. No. 2.1e-280;
0; Mismatches 264;
                                                                                                                                                                                                                                                                        Reed JN,
                                                                                                                                                                                      (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 58-62; 62pp; English
                                                                                                                                                                                                                                                                        Salmeron JM,
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ilarity 80.3%;
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                            CTATACGATTTGGCCCCGAGGTAGATCATCAGATTGTCAAAAGCTGATGTAGCTGGTGGTGGT
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                                                                                   CAACTICALCAGGGGGGGCTCATCCICACTGTCAACGGACAGCACGGTGCTATGGATAT
                                                                                                                                                            GGTAGGCCAAGATGCGGTGATCCGTCTTCCAAGGCGTGCCGTAACGACCCATTCAC
      363 GITACCTATIGGACCTGGTACTGGTCCCGACGACCCAAAGCCTGTAATTCTATIGCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus for reducing and/or preventing the growth of a fungus of the genus for reducing and/or preventing the growth of a fungus of the genus for sarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. Plasmid pAgroTRIr comprises a selectable marker operably linked to a promoter and terminator sequence and the tricothecene resistance gene described in GENBESQ record AAA54206 behind and in frame with the Arabidopsis polyadenylation signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AGCCGAGGGCATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 915.6; DB 21; Length 13737;
Pred. No. 2.1e-280;
0; Mismatches 264; Indels 3;
crop protection; mycotoxin;
heterologous gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13737 BP; 3341 A; 3442 C; 3629 G; 3325 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                      Dawson
                                                                                                                                                                                                                                                                                                                                                      Reed JN,
                                                                                                                                                                                                                                                                                                                GES MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 54~58; 62pp; English.
                fungus; wheat; maize; barley; rice;
transformation; Fusarium; ds.
  resistant;
                                                                                                                                                                                                                                                                                             (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW
                                                                                                                                                                                                                                                                                                                                                      Salmeron JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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ilarity 80.3%;
Conservative 0
                                                                                                                                                                                                                                   99US-0282995.
                                                                                                                                                                                              29-MAR-2000; 2000WO-EP02769
  resistance;
                                                                                                                                                                                                                                                                                                                                                      Peters C,
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-679374/66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 1087; Conserv
                                                                                                                     WO200060061-A2
                                                                                                                                                                                                                                                       11-FEB-2000;
      Tricothecene
                                                                                                                                                                                                                                     31-MAR-1999;
                                                                                                                                                            12-OCT-2000
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                                                                               Synthetic
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Sequence encoding trichothecene resistance polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..1425
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 50-51; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmeron JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.4%;
51.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999; 99US-0282995,
11-FEB-2000; 2000US-0502852.
                                                                              (first entry)
                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-679374/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          barley or rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200060061-A2
                                                                              26-FEB-2001
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                           AAA54210
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958 GGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCGAC 1017 961 GGACTCCCGGAAACGTATCCAGGGTTATTAGTCAACATGACCTTTAATACAGGTTCCCTG 1020 1021 AAAAGCTTGGATCATAAAAGTTTGGGCGTTCTTGCATCACAGATTCGCAGGAAGCTAGAC 1080 ccesacaadactracerracercaaccaarrdaractrarerradaarrardaderc 1200 GTGAAAGACCTCCGCGATGATCCTTCAGCGCCCACGATCGAGGCTATGAGAAAGGCGGGA 315 1321 TCCTCCAGAGGTGAAATGGTGGTTGCTCTTTGCCTTAGAGATAAAGATTGGAAGTGCCTG 1380 838 AGAATGGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTTGATGCTCGACGGCAATG 897 GGTGTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACCATC 957 361 TITCCTATCTACATGTTAGACGAAAAGACTTTTGCGCCTTGCATGACTATCAATCCACCT GAACCCGACACCACGCTAGTTCATGAATAGTGGAAACCTCTAGAAATACAAGTGGAGAG TCCACTGATGATATCGTCACTGCTTTCATCTGGAAATCAGTTTCTCGAGCCCGTTTATCT 370 ATIGGACCIGGIACIGGICCCGACGACCAAAGCCIGIAAIICIATIGCAGCICAACIIC ATCAAGGGCGGACTCATCACTGTCAACGGACAGCACGGTGCTATGGATATGGTAGGC GAAAAGGAACAGTCTTGTTTCGAACTCTACTTGGGCTTATGTTGAATTTTTCTGCTATC TCATTGCAGAATCTGAGGATTTTGGCAATGCAGACATGTACTTCTGGCACAAAATTTGTC 901 CGACTTAAACCAGAAACGAAATCAAATTTAGGGCGTGCTGTGGATGTTAGAAAACGGCTA GGAAACACTATAGGTATGGCCCCAAGAGTGGGCCTGTATTTGCAGTTCAAGCATTT 481 ATCTCCGGCGGCCTCGTCTTAACTATTGTCGGCAGCACAATATTATGGATATAACAGGA CAAGATGCGGTGATCCGTCTACTCTCCAAGGCGTGCCGTAACGACCCATTCACCGAAGAG 541 CAGGAAAGTATCATCAATTAAATCTTGCCACCAAAAACCTTTCTCTGATGAA GAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAAAACTATACG 610 ATT---GGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGTGACGCT GTTCTCACGCCGGTCAGT-----GCAAGCTGGGCGTTCTTCACATTCAGCCCCAAG GCCATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCATCAACAAAGTTCGTG CCCGCGAGCA-----TGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACAAC CCTAAAGTCTTCGATTTGGCCTATAATACATGCGCACTTGCTACGCTCCTTAGCCGATGC CCCGACAAGTCCAACGTATCCCTGACGGCTGATGCGGACCCATCTACCAGCGTCATGCTG 1201 AGTICGIGGGCAAAAGICAGCCIGIAIGACGIIGAITICAAICTAGGGCTIGGGAAGCCC 1261 AAGAGTGTACGACGCCGCCTTCATTTCCCTTGAGAGCCTAATATATTTTATGCCTAGA 1192 GAGACTGTGAGACGGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCAAG 1132 AGTICTIGGGCCAAGGIGGGACTCTGGGATTACGACTTGGGGCTCGGACTGGGTAAGCCC 1252 AAGCCTGATGGCGAGTTCTGTGCGGCGTTTCTCTGAGGGATGAGGATATGGACCGATTG TACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAGGAAGACGTT 316 256 421 430 550 1018 1081 199 299 718 781 778 841 1072 1141 721 qq d à g g 임 g δ Š ò ð g à gg ð g à Dp à 셤 à qq à δ g ò 셤 ð g g ò ò qq à P 5 135 300 123 183 195 255 243 75 A heterologous gene encoding a gene product which confers trichochecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing myclotxin contemination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. 196 AGCGAGGGAAACACGAAGAACTTCCTTTTATCGTCCCTTTTTGAGGACGTTCCTCGTGTTGTA CAGCICGACACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACACCCCAAATCAGTCTC CAACTTGATATTTTGGGACAACAACCTTCGCTATACAACTATACACTCAAATATGCTCT 76 CTCTACCCCGTCTCTGATTCCTCAATATCCCACTATTGTCAGCACCTTCGAGCAAGGT CTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCCAGGTCAAAGCCGAGGCCATT GACGAAGGTAACACTGGTACCTACAGAATTGTCCCGTCAGACAAATTCCAC---TTATC 124 Arcraccergraccagarcerrerecreargaccararceraaraccrraacaagaga CTTGAAACATTGGCTAAAAATTTCCAGTGGCTAGCAGGAAATGTCGTAAATGAAGGTGCT cell for preventing mycotoxin contamination of wheat, maize, y or rice plant, comprises heterologous polynucleotide encoding product expressed in cell, having trichothecene resistance Gaps Tricothecene resistance, resistant; crop protection; mycotoxin; fungus; wheat; maize; barley; rice; heterologous gene; transformation; Fusarium; ds. 27; 21; Length 1425; /*tag= a /product= Trichothecene resistance polypeptide Indels Dawson JL; Score 249.8; DB 21; Pred. No. 1.2e-68; 0; Mismatches 622; Reed JN,

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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of the came genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production to potential of the microraganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be identified and gene copy number variation and stability can be identified and gene copy number variation and stability can be identified and gene copy number variation and stability can be comploquenesis, recombination, metabolic or catabolic pathway morphogenesis, recombination, metabolic or catabolic pathway corrandom cDNA clones including elimination of redundancy as one spot on an expansion of the results. APRILASS represents ESTs from an expersion of the results. AARVATOR to AARVILAT represents ESTs from Aspergillus of AARVILASY represents ESTS from Aspergillus of AARVILASY represents resear, which are all and energing the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                Multiple gene expression; filamentous fungal cell; BST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reseei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olsen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                695 BP; 174 A; 191 C; 156 G; 172 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all specifically claimed in the present invention.
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1312 AAGGCGGATAAGGAGTGGACCAAGTATGC 1340
                       Claim 88; Page 1954-1955; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                Aspergillus oryzae EST SEQ ID NO:4594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
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                                                                                                                                             AAF12071 standard; cDNA; 695 BP
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DB 21; Length 695;

Score 146.2; DB 2. Pred. No. 8.9e-36;

10.8%;

Query Match Best Local Similarity

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TAGGCCAAGATGCGGTGATCCGTCTACTCCAAGGCGTGCCGTAACGACCCATTCACCG 544
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                                                                            65 AAATCAGTCTCCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGCACCT
                                                                                                      166 AAAICTGCCICTTCCGTIC---GAIGCCICATCTGAICACGAGAIAGICAGGACCC
                                                                                                                                                         223 racadaarogccrccaaadacrcrcrccaarrrcccgrcgcrdcagccagaracrca
                                                                                                                                                                                                             283 GTGAAGGCAGCACAACAATCCTGGCACATTCATGATCAAAGGCACTGGGGAAGACTC
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                                                                                                                                                                                                                                                                                             GAAAGGCGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAAGACGT
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                                                   185 CCGAGGGCATTAGCGAGGGAAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGACGTTC
                          CTTTCAAGATACAGCTCGACACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACACCC
 Gaps
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Abe K;
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Mismatches 225; Indels
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N, Gomi
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Kobayashi T, Kitamoto N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGAGGAAATGACGGCCATGAACCT 569
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FOOD RES INST MIN
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  Conservative
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    325;
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The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising to these sequences. The polynucleotides are useful for monitoring the progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for fungal contamination.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1096 ACGCTGATGCGGACCCATCTACCAGCGTCATGCTGAGTTCTTGGGCCGAAGGTGGGACTC 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAGACGGCCAATCTTT 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of expression of specific Aspergillus genes for monitoring the fermentation and growth conditions of the fungus, using DNA probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 GGAGCGAGTTTCAATCCTCGACGGATATTATGATTAGCTCGTGGGCAAGTGTCAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 ACTCCGGTTGAAGGGTTGATTTCATGCCCAAGAGGTCTGATGGCGAGATTGCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    8.6%; Score 116.2; DB 25; Length 482; 60.1%; Pred. No. 2.7e-26;
                                                                                                           Claim 1; SEQ ID NO 3930; 48pp + Sequence Listing; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 482 BP; 131 A; 109 C; 115 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis
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WPI; 2003-046817/04
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                                                                                                                                                                                                                                                                              The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                                                                                                                                                  Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37RV differ -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1016 ACCCGGGAGCATGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACAACCCG
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Pred. No. 8.4;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
                                                                           Venter JC;
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                                                                           Fraser CM,
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Matches 101, Conservative
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24-JUN-1998;
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Mizutani M;

Kusumi T,

Fukui Y,

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Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Suppositio DNA sequences encoding aromatic acyl transferase from different plants are described in AAT37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone, e.g. of flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 61-65; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T, Fujiwara H, Fukui
Tanaka Y, Yonekura K;
                                                                                                                                                                                                                                                                                            96JP-0046534.
95JP-0067159.
95JP-0196915.
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                                                                                                                            22-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen. Wycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
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                                                                                                                                                                                 Venter JC;
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Pred. No. 8.4;
0; Mismatches 102;
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             24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                             1277 ACAATAGGTTTGATGGAATGGTGTATTTGTACCAAGGCAAAAATGGAGGAAGAAGCATTG 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1337 Argregagarragrriggaagcaaargcrargcagagaggriggagaaagaraaagarrcc 1396
                                                                                                                                                                                              1154 TCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAGACGACCCAATCT
                                                                                                                                                                                                                                                               1217 rcaaggriracgacgregarriregargegesaaagccagagagreregaggregrega
                                                                                                                                                                                                                                                                                                                             --CCAAGAAGCCTGATGGCGAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, cytosine methylation, 5'-CpG-3', uracil; cytosine; diagnosis, drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonuclectide for detecting cytosine methylation SEQ ID NO 20283
                                                                DB 17; Length 1605;
                                                                                                                                 Indels
Sequence 1605 BP; 477 A; 319 C; 375 G; 434 T; 0 other;
                                                                                                                                 96;
                                                                                               1.4
                                                                2.7%; Score 36.4; E
51.9%; Pred. No. 1.4;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                   1214 TIGAGCCIGITGAGAGCIIGAIGIACTITAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1331 CCAAGTATGCGCAGTACGTTGGTTAG 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1397 TCATGGAAACTGCTTAATTTGCTTAG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA; 1459 BP.
                                                                                            ilarity 51.9%;
Conservative
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (0) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                     Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                            Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the disclosure of the invention.
                                                                                             01-SEP-2001; 2001WO-EP10074.
                                                                                                                                      01-SEP-2000; 2000DE-1043826.
05-SEP-2000; 2000DE-1044543.
                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                            Piepenbrock
                                                                                                                                                                                                                                                                                                        WPI; 2002-371829/40.
WO200218632-A2
                                                07-MAR-2002
                                                                                                                                                                                                                                                          Olek A,
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2.6%; Score 35.6; DB 24; Length 1459; 49.0%; Pred. No. 2.4; Sequence 1459 BP; 173 A; 200 C; 526 G; 560 T; 0 other; Query Match

1108 ccaaatricececcaacicceaccecaacitracaccececececaaaareeceaaa 1049 CCCCGTCTCTGATTCCTCAATATCCCACTATTGTCAGCACCTTCGAGCAAGGTCTTAA 140 200 1048 caccececraaaceaceaaaarraarcrerececececriraaaaceceaaaeeca 989 988 AĊĠAAŤĊĠAACAACĊĠAAAĊĠĊĠŢĊŢŢĊĠĊĠAAŢĊŢĀĀAAĊĠĀĠAĀŢĊĠĀĠĀ 929 80 CGACACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACACCCAAATCAGTCTCCTCTA GCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAAAGCCGAGGGCATTAGCGA Gaps 0; Indels 66 0; Mismatches 201 GGGAAACACAGGAA 214 928 CCGAAAAAAACGAA 915 Conservative Local Similarity les 95; Conserv 81 141 Best Loca Matches 셤 g В ò ð à

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RESULT 13
     ABQ33693
ID ABQ3
XX
AC ABQ2
XX
DT 12-i
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ABQ33693 standard; DNA; 1459

(first entry)

12-JUL-2002

ABQ33693;

Oligonucleotide for detecting cytosine methylation SEQ ID NO 20284.

Human, cytosine methylation, 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Ношо

WO200218632-A2

07-MAR-2002

Guetig D;

01-SEP-2001; 2001WO-EP10074.

01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543.

(EPIG-) EPIGENOMICS AG.

Guetig Berlin K, Piepenbrock C, Olek A,

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA

Claim 12; 56pp + Sequence Listing; 56pp; German.

methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic Cytosine (C) but not methylated C to uracil, then part of the genomic C The amplicon is the target C is amplified to form a labeled amplicon. The amplicon is hybridisation to both classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory Systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the methylation for defremining the degree of cytosine methylation described in the disclosure of the invention.

Sequence 1459 BP; 560 A; 526 C; 200 G; 173 T; 0 other;

Gaps 0; Score 35.6; DB 24; Length 1459; Pred. No. 2.4; 0; Mismatches 99; Indels 0: 99; Indels .6%; 49.0%; 95; Conservative Local Similarity Query Match Matches

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81 CCCCGTCTCTGATTCCTCTCTATATCCCACTATTGTCAGCACCTTCGAGGTCTTAA 140

CACCGCGCGTAAACGACCAAAATTAATCTCTACCCCGCGCTTTAAAACCCCGAAACGCA 471 141 GCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAAAGCCGAGGGCATTAGCGA 412

472 ACGAATCGAACAACCCGAAACGCGCGTCTTCCGCGAATCTAAAAACGACGAAATCGACGA 531

201 GGGAAACACAGGAA 214

532 CCGAAAAAAACGAA 545

214

201 GGGAAACACAGGAA

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838 CCGAAAAAAACGAA 825

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Oligonucleotide for detecting cytosine methylation SEQ ID NO 1034.

(first entry)

12-JUL-2002

ABQ14443;

ABQ14443 standard; DNA; 1463 BP.

RESULT 15 ABQ14443

141 GCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAAAGCCGAGGGCATTAGCGA

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic C DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue companies investigating cell differentiation. The method allows the methylation status of many C residues to be determined simmltaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the control of the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                                                                                                                                                                                                Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                          Oligonucleotide for detecting cytosine methylation SEQ ID NO 1033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 1463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guetig D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K,
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                                 ABQ14442 standard; DNA; 1463 BP.
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                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-371829/40.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      WO200218632-A2.
                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                         12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2002
                                                                               ABQ14442;
RESULT 14
                   ABQ14442/
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert conve Claim 12; 56pp + Sequence Listing; 56pp; German. the disclosure of the invention.

useful of

Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -

'n

Guetig

Berlin K,

Piepenbrock C,

olek A,

WPI; 2002-371829/40.

(EPIG-) EPIGENOMICS AG.

01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543. 01-SEP-2001; 2001WO-EP10074

WO200218632-A2. Homo sapiens.

07-MAR-2002.

Length 1463; Seguence 1463 BP; 553 A; 521 C; 200 G; 189 T; 0 other; DB 24; Score 35.6; DE Pred. No. 2.4; 2.6%; Query Match. Best Local Similarity

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Gaps

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99; Indels

Pred. No. 2.4; 0; Mismatches

49.08;

95; Conservative

Matches

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1018 cchahtricececchacteceaceceaetrinacheececececeaeharicecheae 959 -81 CCCCGTCTCTGATTCCTCTAATATCCCACTATTGTCAGCACCTTCGAGCAAGGTCTTAA 140

21 CGACACCCTCGGCCAGCTACCAGGCCTTCTTCGATCTACACCCCAAATCAGTCTCTTA

0;

0; Mismatches 99; Indels

Matches 95; Conservative

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446 CCAAATTCGCGCCCAACTCCGACCCCAGTTTACACCCCGCCCCGAAATCCCCAAA 505
                                                                  81 CCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGCACCTTCGAGCAAGGTCTTAA 140
                                                                                      141 GCGCTTCTCCGAAGCCGTCCCATGGGTCGCCAGGTCAAAGCCGAAGAGGGCATTAGCGA 200
                                                                                                                                         21 CGACACCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACACCCCAAATCAGTCTCTCTA 80
0; Gaps
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7, 2004, 17:54:07; Search time 5222 Seconds (without alignments) 10623.028 Million cell updates/sec 1 atggctttcaagatacagct.....atgcgcagtacgttggttag 1356 5777422 Total number of hits satisfying chosen parameters: 2888711 seqs, 20454813386 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0
Maximum DB seq length: 2000000000 US-10-614-954-5 1356 gb_htg:,,
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B 1 (bases 1 to 1356)
S Hohn,T.M., Peters,C. and Salmeron,J.
Trichotheone-Resistant transgenic plants
AL Patent: US 6346655-A 5 12-FEB-2002;
Location/Qualifiers

REFERENCE AUTHORS TITLE JOURNAL FEATURES

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAKIES # Soult Query No. Score Match Length DB ID Description	Inditional	33 AR193433	1340 98.8 1605 8 AB000874 AB000874	1340 98.8 3003 8 AB009607 AB009607	1340 98.8 8646 8 AB011417 AB011417	1334 98.4 1336 8 AFZ126US AFZ126US 1334 98.4 1336 8 AFZ126US	1330.8 98.1 1336 8 AF212603 AF212603	1330.8 98.1 1336 8 AF212606 AF212606	1330.8 98.1 1336 8 AF212607 AF212607	1329.2 98.0 1336 8 AF212602 AF212602	1329.2 98.0 1336 8 AF212604 AF212604	1321.2 97.4 1336 8 AF212582 AF212582	1321.2 97.4 1336 8 AF212583 AF212583	1321.2 97.4 1336 8 AFZ12584 AFZ12584 1321.2 97.4 1336 8 AFZ12585	1321.2 97.4 1336 8 AF212586 AF212586	1321.2 97.4 1336 8 AF212587 AF212587	1319.6 97.3 1336 8 AF212594 AF212594	1319.6 97.3 1336 8 AF212601 AF212601	1318 97.2 1336 8 AFZ1Z595 AFZ1Z595 1318 97.2 1336 8 AF212596	1318 97.2 1336 8 AF212597 AF212597	1318 97.2 1336 8 AF212598 AF212598	1318 97.2 1336 8 AF212599 AF212599	1316.4 97.1 1336 8 AFZ12600 AFZ12600 AFZ12600	1314.8 97.0 1336 8	1304.4 96.2 1322 8 AY222642 AY222642	1304.4 96.2 1322 8 AY225882 AY225882	1303.6 96.1 1336 8 AF212591 AF212591	1303.6 96.1 1336 8 AF212592 AF212592	1303.6 96.1 1336 8 AF212593 AF212593	1287.9 53.0 1336 8 AF212612 AF21261	1282.8 94.6 1336 8 AF212613 AF212613	1281.2 94.5 1336 8 AF212611 AF212611 Fusar	1270 93.7 1336 8	1247.6 92.0 1336 8 AF212615 AF212615	1247.6 92.0 1336 8 AF212616 AF212616	1247.6 92.0 1336 8 AF212617 AF212617 Fusar 1247.6 92.0 1326 9 AF212619	915.6 67.5 1403	ALIGNMENTS	SULT 1 193433	Z		JESSION AR193433 SZION AR194433.1 GT-20234348
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1356 385 c 349 g 303 t 100.0%; Score 1356; DB 6; Length 1356; 100.0%; Pred. No. 0;	Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 AIGGCTTTCAAGATACAGCTCGACACCCTCGGCCAGCCTCCTTTCGATCTAC 60 DD 1 AIGGCTTTCAAGATACAGCTCGACACCCTCGGCCAGCCTACCAGGCCTCCTTTCGATCTAC 60	OY 61 ACCCAAATCAGICTCCTCTACCCGGTCTCTGATTCCTCTCAGTATCCCACTATTGTCAGC 120	QY 121 ACCTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTC 180		QY 241 GTTCCTCGTGTTGTAGTGAAAGACCTCCGCGATGATCCTTCAGCGCCCACGATCGAGGGT 300 241 GTTCCTCGTGTTGTAGTGAAAGACCTCCGCGATGATCCTTCAGCGCCCACGATCGAGGGT 300	Qy 301 ATGAGAAAGGGGGATACCCTATGGGATGTTTGACGAGAACATCGTGGCCAAGGAAG 360	OY 361 ACGTTACCDAITGGACCTGGTACTGGTCCCGACGACGCCTGTAATTCTATTGCAG 420	OY 421 CTCAACTTCATCAAGGGGGGCTCATCTCATCAACGGACAGGGGGGTATGGAT 480	OY 481 ATGGTAGGCCAAGATGCGTGATCGTCTACTCTCCAAGGGTGCGTAACGACCCATTC 540	OY 541 ACCGAAGAAATGACGGCCATGAACCTCGATGACGACGATAGTTCTTACCTTGAA 600	QY 601 AACTATACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGT 660	OY 661 GACGCTGTTCTCACGCCGGTCAAGCTGGGCGTTCTTCACATTCAGCCCCAAGGCC 720	Qy 721 AIGTCAGAGCICAAGGAIGCIACCAAGACICITGACGCAICAAAAGTICGIGICG 780	QY 781 ACTGACGATGCTCTTTCGGCGTTCATCTGGAAATCGGCCTCTCGGGGGCGTCTCGAAAGA 840	OY 841 ATCGATGGCTCTGCCCACCGGGTTCTGCCGTGCTGTTGATGCTCGGCAATGGGT 900	ON 901 GTCTCGAACTACCCAGGCCTTCTTCAAAACATGACCTACCACCATCGACCATGGC 960 -

Db 1155 GCGAGCATGCGCAAGCGAACCAGTACCTGCACAACAACAACAAGCTTTGG 1214 Qy 1081 TCCAACGTATCCTGACGGTGACGACCCATCTACCAGCGTCATGCTGGTTTTTGG 1140 Db 1215 TCCAACGTATCTTGACGACTTTGGGACCCATCTACCAGCGTCATGCTGAGTTCTTTGG 1274 Qy 1141 GCCAAGGTCGGACTTTGGACTTTGGGCTCGGCTCAGGTAAGCCTGTG 1200 Db 1275 GCCAAGGTCGGAATTACGACTTTGGGTTCGGTAAGCCCGAGACTGTG 1334 Qy 1201 AGACGGCCAATCTTTGAGGCTTTGGGTTCGGACTGGGTAAGCCCAAGAAGCTTGAT Db 1335 AGACGGCCAATCTTTGAGGCTTTGAGAGCTTGATGTTTATGCCCAAGAAGCCTGAT 1394 Qy 1261 GGCCAGTTCTTGAGGCTTTTGAGAGCTTGATGTTTATGCCCAAGAAGCCTGAT 1394 Db 1395 GGCAGTTCTTGTGGCGCCTTTTTTTTTTTTTTTTTTTTT	RESULT 4 AB009607 LOCUS Gibberella zeae genes for UTP-ammonia ligase and trichothecene 3-O-acetyltransferase, partial and complete cds. ACCESSION VERSION VERSION VERSION Tril01; trichothecene 3-O-acetyltransferase; UTP-ammonia ligase. SOURCE Gibberella zeae Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella. REFERENCE AUTHORS Kimura,M., Shingu,Y., Yoneyama,K. and Yamaguchi,I. Features of Tril01, the trichothecene 3-O-acetyltransferase gene, TITLE TITLE Features of Tril01, the trichothecene 3-O-acetyltransferase gene, TITLE Features of Tril01, the trichothecene 3-O-acetyltransferase gene, Biosci. Biotechnol. Biochem. 62 (5), 1033-1036 (1998)	φ	/procedum_de=BAAA59350-1 /db_xxef=Ga1:3252782" /translation="LEKAGLSLTSMDDGGVRVETIELKDHPFFVGLQAHPBYKSKTLA_PAPSLIGLNAASSGGLDEIIEAAHKKQSSSNGVSDVINF" polyA_signal 39740.2 gene
Best Local Similarity 99.3%; Pred. No. 0; Indels 0; Gaps 0; Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0; Ostatorial 0; ArcGCTTTCAAGATACAGCTCCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTAC 0	301 ATCAGAAAGGCGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAAG 435 ATCAGAAAGGCGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAAG 361 ACGTTACCTATTGGACCTGGTACTGGTCCCGACGACCCTAAAGCCTGTAATTCTATTGCAG 425 ACGTTACCTATTGGACCTGGTACTGGCCCGACGACGACCTGTAATTCTATTGCAG 426 ACGTTACCTATTGGACCTGGTACTGGCCCGACGACGACGTGCTATTGCAG 427 CTCAACTTCATCAAGGGCGGACTCATCCTCACTGTCAAGGCCTGCAGTGTATTGTATTGCAG 428 ATGGTAGCCAAAGAGCGGACTCATCCTCACTGTCATTGAACGACCGGTGCTATGGAT 481 ATGGTAGCCAAAGAGCGGACTCATCCTCACTCCAAGGCGTGCCGTAACGACCATTC 615 ATGGTAGGCCAAGATGACGGTCATCCTCACTCCCCAAAGGCGTGCCGTAACGACCCATTC 615 ATGGTAGGCCAAGATGACGGTCATCCGTTACTCTCCAAAGGCGTGCCGTAACGACCCATTC 616 ATGGTAGGCCAAAGATGACGGTCATCCTCCAAAGGCGTGCCGTAACGACCCATTC 617 ATGGTAGGCCAAAGATGACGGCTCATCCTCCAAAGGCGTGCCGTAACGACCCATTC 618 ATGGTAGGCCAAAATGACGGCCATGAACCTCTCCAAAGGCGTGCCGTAACGACCCATTC 619 ATGGTAGGCCAAAATGACGGCCATGAACCTCCCAAAGGCGTGCCGTAACGACCCATTC 611 ATGGTAGGCCAAAATGACGGCCATGAACCTCTCCAAAGGCGTGCCGTAACGACCCATTC 611 ATGGTAGGCCAAAAATGACGGCCAATGAACCTCCCAAAGCCGTAACGATCCTTACCATTGAA 611 ATGGTAGGACAAAATGACGGCCAATGAACCTCCCAAAGACGATAGTTCCTTAACCTTGAAA 612 ATGGTAGAAGAAGAATGACGGCCAATGAACCTCCAAAGACGAAAAATGACGACCCATTCCAAAGACGAAAAACAACGAACAAACCCAATTCCAAAAAAAA	Db 675 Accdandadedandadededededededededededededede	841 ATGGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTTGATGCTCGACCG

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Location/Qualifiers

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/organism="Gibberella zeae"
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Gibberella zeae genes for trichothecene 3-O-acetyltransferase, UTP-ammonia ligase and phosphate permease, complete cds.
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PEBS Lett. 435 (2-3), 163-168 (1998)
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note="Tril01 mRNA is reported under AB000874
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RERKLPYLGTCLGMQTAVIEYARNVMGLKGATSBERGATSAGRUNDVAKWA
RERKLPYLGTCLGMQTAVIEYARNVMGLKGATSBERGATSAGRUNDVAKWA
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/db_xref="taxon:5518"
/db_xref="taxon:5
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IMGVGIGGDYPLSSIITSEFATTKWRCAMMAAVFAMQGIGQLVAALVMMFLTLGFKSS
LEQAADTKSCTGDCQIAVDKMWRTLVGFGAVPACIALYYRLTIPETPRYTFDVARDVB
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PNTTTFIYDGBYFPTRYRSTGBIGISAASGKIGSIIGQGAISILRTHGATDKNEAÞWMD
HYLEIYALFWILGIFTTLLIPETARKTLEELSGEDDYANHDHALESETQASHDKARRT
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apfgwyhvracivagygfftdsydifcvsmltimlgivyypgkgklptssdnaiklst
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/protein_id="BAA33769.1"
/db_xref="GI:3724291"
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                                                                                                                           GTTCCTCGTGTTGTAGTGAAAGACCTCCGCGATGATCCTTCAGCGCCCACGATCGAGGGT
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GLKRESEAVPWYAGOVKARGTSEGNTGTSFTVPFEDVPRVVVKDLRDDPSAPT1EGNR
KAGYPWAMFDBNI1APKKTP1GPGTGPDDPKPVILLQLNFIKGGLILTVNGQGRAMD
MYGQDAVIRLLSKACKNDPFTEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVA
GGDAVLTPVSASWAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRV
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RSELDPASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGL
GLGKPETVRRPIFEPVESLMYFWPKKPDGEFCAALSLRDEDMDRLKADKEWT"
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycelidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 1336)
0'Donnell,K., Kistler,H.C., Tacke,B.K. and Casper,H.H.
Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Pusarium graminearum, t
                                                       GGCGAGTTCTGTGCGGCGCTTTCTCTGAGGGATGAGGATATGGACCGATTGAAGGCGGAT
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Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
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/product="trichothecene 3-0-acetyltransferase"
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/protein_id="AAG43712.1"
/db_xref="GI:12003707"
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O'Donnell,K.
Direct Submission
Submitted (18-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 616
Location/Qualifiers
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Sibberella zeae strain NRRL28063 trichothecene
--O-acetyltransferase, partial cds.
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/mol_type="genomic DNA"
/strain="NRRL28063"
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iive 0; Mismatches
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                                                        AAAGCCGAGGCATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC
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GLKRESEAVPWYAGOVKAEGISEGWYGTSFIVPFEDVPRVVVKULRDDSSAPTIEGMR
KAGYPMAMFDENI IAPRKILPI GGGTGPDDPKPVILLGLINFIKGGLI LITVNGGHGAMD
WYGQDAVIRLLSKAGKNDPFTBEEMTAMNLDRKTI VPYLENYTI GFEVDHQI VKEDVA
GGDAVLTPVGASWAFFTFSPRAMSELKDAATKTLDASTKFVSTDDALSAFIHKSASRV
RLERI DGSAPTEFCRAVDRPAMGVSNNY FGLLGWMTYHSTTGEIDARSLGATASRL
RSELDPASMGQRTGLAYYLHNNIPKSNYSTADADPSTSWLLSSMAKVGLMDYDFGI
GLGKRETVRRPIFERCAATLANYLHNIPKSNYSTADADPSTSWLLSSMAKVGLMDYDFGI
GLGKRETVRRPIFERVESLMYFMYERDGEFCAALSLRDEDMDRLKADKEWT"
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                                                      GGCGAGTTCTGTGCGGCGCTTTCTCTGAGGATGAGGATATGGACCGATTGAAGGCGGAT
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Hypocreomycetidae, Hypocreales; Nectriaceae, Gibberella.
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/protein_id="AAG43710.1"
/db_xref="GI:12003703"
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O'Donnell,K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 616
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larity 99.9%; Pred. No. 0;
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/mol_type="genomic DNA"
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1 (bases i to 1336)

0 'Donnell,K., Kistler,H.C., Tacke,B.K. and Casper,H.H.
Gene genealogies reveal global phylogeographic structure and reproductive isolation among lineages of Fusarium graminearum, the fungus causing wheat scab

Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
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O'Donnell,K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 616
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1 (bases 1 to 1336) Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 1336) Hypocreales; Nectriaceae; Gibberella.

2 (brownell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.

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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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O'Donnell,K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
Location/Qualifiers
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/product="trichothecene 3-0-acetyltransferase"
3. .>1336
3. .>1336
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0; Mismatches

    1336
    /organism="Gibberella zeae"
/mol_type="genomic DNA"
/strain="NRRL28436"

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Db 123 ACCTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTC 182	Oy 181 AAAGCCGAGGGCATTAGCGAAGGAAACACACAAACTTCCTTTATCGTCCTTTTGAGGAC 240 Db 183 AAAGCCGAGGGCATTAGCGAAGGAAACACAGGAAACTTCCTTTTATCGTCCTTTTGAGGAC 242	QY 241 GTTCCTCGTCTTGTAGTGAAAGACCTCCGCGATGATCCTTCAGCGCCCACCATCGAGGGT 3 00 Db 243 GTTCCTCGTGTTGTAGTGAAAGATCTCCGCGATGATCTCTTCAGCGCCCACGATCGAGGGT 302	OY 301 ATGAGAAAGGGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCCAAGGAAG 360 DD 303 ATGAGAAAGGGGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAGGAAG 362	Oy 361 ACGITACCTATIGGACCTGGTACTGGTCCCGACGCCCAAAGCCTGTAAITCTATIGCAG 420	Qy 421 CTCAACTTCATCAAGGCGGACTCATCCTCACTGTCAACGGACAGCACGGTGCTATGGAT 480	OY 481 AIGGIAGGCCAAGAIGCGGIGAICCGICIACTCICCAAGGGGGGCGIAACGACCCAIIC 540 DD 483 AIGGIAGGCCAAGAIGCGGIGAICCGICIACTCCCAAGGCGIGCGGAACGACGACTTC 542	Qy 541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA 600 Db 543 ACCGAAGAAATGACGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA 602	Qy 601 AACTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGT 660	Oy 661 GACGCTGTTCTCACGCCGGTCAGTGCAAGCCTGGGGCGTTCTTCACATTCAGCCCCAAGGCC 720 Db 663 GACGCTGTTCTCACGCCGGTCAGTGCAAGCTTGGGCGTTCTTCACATTCAGCCCCAAGGCC 722	721	Qy 781 ACTGACGATGCTCTTTCGGCGTTCATCTGGAAATCGGCCTCTCGCGTGCGT	OY 841 ALGAIGGCICIGCACCTACGAGTICIGCGGTGCTGTTGAIGCTGGCGACCGGCAAIGGGT 900 DD 843 ALGAIGGCTCIGCACCTACGAGTICIGCCGIGCTGTTGAIGCTCGACCGGCAAIGGGT 902	Qy 901 GTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACATCGGC 960	Qy 961 GAAATGGCCAAGGAGTGACTGGGGGCAACAGCATGAGGCGTTGGTTG	Oy 1021 GCGAGCATGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACCACCACAAG 1080	Qy 1081 TCCAACGTATCCTGACGGCTGATGCGGACCCATCTACCAGCGTCATGCTGAGTTCTTGG 1140	Qy 1141 GCCAAGGTGGGATTACGACTTTGGGGTCGGACTGGGTAAGCCCGAGACTGTG 1200	Oy 1201 AGACGGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTTTTATGCCCAAGAAGCCTGAT 1260
AGACGGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCAAGAAGCCTGAT 126	1261 GGCGAGTICTGGGCGCGTTTCTCTGAGGGATGGGAGGAGGGGGATTGAGGGGGAT 1322 1263 GGCGAGTTCTGTGCGGCGCTTTCTCTGAGGGATGAGGGCGGATTGAAGGCGGAT 1322	ANGGAGTGGACCAA	RESULT 15 AF212584 1336 bp DNA linear PLN 26-JUN-2001 DEFINITION Gibberella zeae strain NRRL29010 trichothecene	3-0-acetyltransferase, partial cds. ACCESSION AF212584 VERSION AF212584.1 GI:12003664	KEYWORDS Gibberella zeae SOURCE Gibberella zeae ORGANISM Gibberella zeae Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				JOURNAL Submitted (08-DEC-1999) Microbial Properties Research, NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA FEATURES Location/Qualifiers 1, 1336	/org /mol /str /db	mRNA <3>1336 /product="trichothecene 3-0-acetyltransferase" 3>1336 /codon start=1	<pre>/product="trichothecene 3-0-acetyltransferase" /protein id="AAA43491.1" /db xref="GI:12003665" /translation="MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDPSQYPTIVSTFEQ</pre>	GLKREPSEAVPWVAGOVKAEGISEGNIGTSFIVPFEDVPRVVVKDIRDDPSAPTIEGMR KAGYPMAMFDENII APRKTIPIGPGTGPDDPSPVILLGINFIKGGLILTVNGHHGAMD WVGQDAVIRLISKACRNDPFTEEEBMYAMILDRKTIIVPYLIANYTIGPEVDHQIVRPDVA GGDAVLIPVSASWAPFTFSPKAMSELKDAATKTI.DASTKFVSTDDALSAFIWKSASRV	RIERLIOSAPTERCRAUDARDAGOSNIT PGLLONMITHINSTIGLANBELGATASKL RSELDPASMRQFIRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGF GLGKRETVRRPIFEPVRSKYDGEFCAALSLRDEDMDRLKADKEWT" BASE COUNT 316 a 384 c 296 t	y Match 1321.2; DB 8; Length 1336; Local Similarity 99.4%; Proceed, No. 0; hee 1326. Conservative 0. Mismarches R. Indels 0.	AAGATACAGCTCGACCTCGGCCAGCTACCAGCCTCCTTTCGATCTAC 60	ACCCAAATCACTCTCTCTCTCTCTCTCTCTCTCTCTCAATATCCCACTATTGTCACCTCTCACTATTGTCACCTCTCACTCTCTCT	62* ACCCAAATCAGTCTCCTCTACCCCGTCTCTGATCCTCTCTCAAATATCCCACTATTGTCAGC 122 121 ACCTTCGAAGGTCTTAAAGGGCTTCTCCGAAGCCGTCCCATGGGTTCGAGGCCAGGTC 180

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1203 AGACGGCCAATCTTTGAGCCTGTTGAGGCTTGATGTACTTTATGCCCAAGAAGCCTGAT 1262
                   Search completed: February 7, 2004, 20:53:19 Job time : 5224 secs
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us-10-614-954-6.rag

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OM protein - protein search, using sw model

February 7, 2004, 21:53:49; Search time 553 Seconds (without alignments) 129.450 Million cell updates/sec Run on:

US-10-614-954-6 Title:

1 MAFKIQLDTLGQLPGLLSIY......BDMDRLKADKEWTKYAQYVG 451 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1107863 Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Trichothecene resi	F. graminearum tri	Trichothecene resi	Sequence encoding	Arabidopsis thalia	Arabidopsis thalia	Wheat stress resno	Arabidopsis thalia	Arabidopsis thalia
	ai .	AAB03935	AAY51848	AAB03934	AAB03936	AAG18711	AAG18710	ABU58179	AAG18709	AAG48446
	DB	21	21	21	21	21	21	24	21	21
	Match Length DB ID	451	451	459	474	424	433	436	450	424
Query	Match	100.0	99.1	79.7	41.2	7.3	7.3	7.3	7.3	7.3
C	Score	2334	2314	1860.5	962.5	170.5	170.5	170.5	170.5	169.5
Result	0 1	1	7	Э	4	ហ	φ	7	α	σ

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AAG48445	ABB93749	AAG48444	ABU58173	ABU58177	ABB93641	AAB36457	AAG24209	AAG24208	AAW04724	ABB92609	ABB92606	ABB92608	ABB92607	AAG46685	ABB93668	AAG46684	ABB93310	AAG37720	AAG37735	ABB93930	AAG37734	AAG37719	AAE00254	ABB91119	AAG46686	AAG21060	ABB93980	AAG21059	AAR47475	AAR46929	AAG25750	AAG45712	AAG45711	ABB33588	AAE00240
21	23	21	24	24	23	21	21	21	17	23	23	23	23	21	23	21	23	21	21	23	21	21	22	23	21	21	23	21	15	15	21	21	21	23	22
433	433	449	446	439	442	431	428	440	448	459	450	648	443	441	441	457	475	426	426	426	438	442	448	436	327	448	448	455	448	448	313	479	484	484	439
7.3	7.3	•	٠	6.9	6.7	•	9.9	9.9	6.5	6.5	6.4	6.4	6.3	•	•	•	•	6.1	•		•	6.1	•	•	5.9	5.8	٠	5.8	•	5.7	•	٠	5.7	5.7	5.7
69	69	169.5	168.5	191	156.5	154.5	154		151.5	151.5	49	149	146	4	143	4	4	ζ,	42.	42.	42.	•	4	ή.	٠	4	134.5	•	134	m	32.	32.		ď	132
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAB03935 standard; Protein; 451 AA. (first entry) 26-FEB-2001 AAB03935; RESULT 1 AAB03935 A CONTRACTOR AND A CONT

Trichothecene resistance polypeptide.

Tricothecene resistance; resistant; crop protection; mycotoxin; fungus; wheat; maize; barley; rice; heterologous gene; transformation; Fusarium.

Pusarium graminearum

WO200060061-A2.

12-OCT-2000.

29-MAR-2000; 2000WO-EP02769.

31-MAR-1999; 99US-0282995. 11-FEB-2000; 2000US-0502852.

(NOVS) NOVARTIS AG. (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

Dawson JL; Salmeron JM, Reed JN, Hohn IM, Peters C,

WPI; 2000-679374/66. N-PSDB; AAA54209.

02-FEB-2000

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                                                                                                                              A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus Fusarium that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAEGISEGNIGISFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK
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          Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance
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                                                                                                                                                                                                                                                                                                                                       100.0%; Score 2334; DB 21; Length 451; 100.0%; Pred. No. 5.4e-211; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            graminearum trichothecene 3-0-acetyltransferase protein.
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                                                                                                   Claim 15; Page 49-50; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                               Matches 451; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                          451 AA;
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                                                                                                                                                                                                             This invention describes a novel protein with trichothecin 3-0-acetyltransferase activity. The gene is used as a selective marker in a gene manipulation using eukaryote as the host cell. This sequence represents the trichothecin 3-0-acetyltransferase isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                          TEEEMIAMNLDRKIIVPYLENYTIGPEVDHQIVKPDVAGGDAVLTPVSASWAFFKESPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 MSELKDATKTLDASTKFVSTDDALSAFIWKSASRVKLERIDGSAPTEFCRAVDARPAMG
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                                                                                                                                                                                                                                                                                                                                                                      1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV
                                                                                                                                                Trichothecin 3-O-acetyltransferase gene useful as a selective marker gene manipulations in eukaryotic host cells -
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                    Length 451;
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                                                                                                                                                                                                                                                                                                                   Score 2314; DB 21;
Pred. No. 4.2e-209;
0; Mismatches 4;
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                        98JP-0200280.
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                                                                     RIKAGAKU KENKYUSHO.
YAMAGUCHI I.
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                     Fusarium graminearum
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447; Conserv
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                        15-JUL-1998;
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Best Local S
Matches 447
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Best Local S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 TEGISEGNIGISKIIPYEETPRLVVKDLRDDSSAPTIEGLRKAGFPLEMFDENVVAPRKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 SSTYPGLLQNMTYHDSTVAEIANEPLGATASRLRSELNSDRLRRRTQALATYMHGLPDKS
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                                                                                                                                                                                                                                                                      Dawson JL;
fungus; wheat; maize; barley; rice; heterologous gene;
                                                                                                                                                                                                                                                                      Reed JN,
                                                                                                                                                                                                                    (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 46-48; 62pp; English.
                                                                                                                                                                                                                                                                      Salmeron JM,
                                                                                                                                          29-MAR-2000; 2000WO-EP02769.
                                                                                                                                                                       31-MAR-1999; 99US-0282995.
11-FEB-2000; 2000US-0502852.
                                              Fusarium sporotrichioides
              transformation; Fusarium.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant cell for preventing mycotoxin contamination of wheat, maize, barley or rice plant, comprises heterologous polynucleotide encoding gene product expressed in cell, having trichothecene resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding trichothecene resistance polypeptide.
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MEH.
                                422 EFCAALSLRDEDMDRLKADKEWTKYAQYVG
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         201 ELLIGNIDKSKSIPLFDE-TWEPDTTLVHEIVETSRNTSGEEKEQSCSSNSTWAYVEFSA 259
                                                             MGVSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRSELDPA--SMRQRTRGLATYLHN 356
                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                           357 NPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMP
                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 20229.
                                                                                                                                   KKPDGEFCAALSLRDEDMDRLKADKEWTKYAQYVG 451
                                                                                                                                                                             AAG18711 standard; Protein; 424 AA.
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7.3%; Score 170.5; DB 21; Length 424;
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Plant; EST; expressed sequence tag; stress response; drought;

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Pred. No. 4.8e-07,
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ABU58179 standard; Protein; 436 AA

Wheat stress response protein #7.

(first entry)

14-APR-2003

ABU58179

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DT 14-A
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The invention relates to isolated nucleic acids encoding plant stress response proteins (including peptide-methionine sulphoxide reductases) appearing as ABU58148-ABU58246 (or a protein 80% identical to them) from Zea mays, Oryza sativa, Glycine max, or Triticum aestivum. Also included are expression cassettes, transformed host cells, transgenic plants/seeds, modulating the level of peptide-methionine sulphoxide reductase in a plant and a computer system/data enthionine processing system for identifying, analysing, or modelling a genetic sequence. The plant nucleic acid is useful in developing strategies to improve plant response to stress (e.g. drought, heat, radiation or pathogen attack), engineering plants with increased disease and stress resistance, manipulating DNA repair and recombination efficiency, manipulating intracellular protein transport, and improving/protecting grain flavour. The nucleic acids may also be used as probes or amplification primers in the detection, quantitation or isolation of gene transcripts, for recombinant expression of encoded polypeptides, as immunogens in preparing or screening antibodies, and in sense or antisense suppression of one or more genes in a host cell, tissue or plant. The proteins may be used as immunogens or antigens to obtain antibodies specifically immunoreactive with the protein, and in assays for enzyme agonists or antagonists. The present sequence is a plant stress response protein (or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide-methionine sulfoxide reductase and nucleic acids, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated nucleic acids encoding plant stress
             heat; radiation; pathogen attack; grain flavour; disease resistance; peptide-methionine sulphoxide reductase; DNA repair; enzyme; intracellular protein transport.
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Weng Z;
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99US-133436P.
99US-133437P.
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99US-137667P.
2000US-0566394.
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ODELL J T.
RAFALSKI J A.
THORPE C J.
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WENG Z.
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Thorpe CJ,
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                                                                                                                                                                                                NESLGATASRLRSELDPASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKV 383
                                                                                                                                                                                                                 318 SQPLGYVADTIRKAVDHVD-DAYTRSVIDYLEVESEKGSQAARGQIMPESDLWVVSWLGM 376
                 56 VACQVKAEGISEGN----TGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMA 109
                                                    110 MFDENIIAPRKTLPIGPGTGPDDPKPVILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVI 168
                                                                                        RL-----LSKACRNDPFTEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAG 219
                                                                                                                           GDAVLTPVSASWAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWK------ 271
                                                                                                                                                            ---SASRVRL-----ERIDGSAPTEFCRAVDARPAMGVSNNYPGLLQNMTYHNSTIGEIA 323
                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                               61; Mismatches 158; Indels 109; Gaps
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                                                                                                                                                                                                                                              384 GLWDYDFGLGLGKPETVRRPIFEPVESLMYFMPKKPDGEFCAALSLRDEDMD
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99US-0132485.
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23-MAR-1999;
25-MAR-1999;
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16-APR-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                Arabidopsis thaliana
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UUS-0139459 UUS-0139460 UUS-0139461 UUS-0139462 UUS-0139462 UUS-0139462 UUS-013962 UUS-0139839 UUS-0140353 UUS-0140353 UUS-0140953 UUS-0140953 UUS-0140953 UUS-0140953 UUS-0140953 UUS-0140953 UUS-0140953 UUS-0140953	990S-01410842. 990S-0142055. 990S-0142803. 990S-0142903. 990S-0142977. 990S-014397. 990S-0144085. 990S-0144085. 990S-0144331. 990S-0144332. 990S-0144333. 990S-0144333. 990S-0144333. 990S-0144333. 990S-0144334. 990S-0144334. 990S-0145088. 990S-0145088. 990S-0145088. 990S-0145088. 990S-0145088. 990S-0145088. 990S-0145088.	905.0145918 905.0145918 905.0145918 905.0145918 905.0146386 905.0147204 905.0147204 905.0147204 905.0147305 905.0147405 905.0147405 905.0147406 905.0147406 905.0147406 905.0147406 905.0148119 905.0148141 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341 905.0148341
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DB 21; Length 433; Query Match 7.3%; Score 169.5; DE Best Local Similarity 23.0%; Pred. No. 6e-97; Matches 105; Conservative 61; Mismatches 1 9908-0159293. 9908-0159294. 9908-0159295. 9908-0159330. 9908-0159330. 99US-0159637. 99US-0159638. 99US-0159584. 99US-0149902. 99US-014930. 99US-015084. 99US-015084. 99US-0151065. 99US-0151080. 99US-0151303. 99US-0151338. 99US-0151338. 99US-0153339. 99US-0155486. 99US-0155659. 99US-0156458. 99US-0156596. 99US-0157117. 99US-0157753. 99US-0157865. 99US-0158029. 99US-0158232. 99US-0158369. 99US-0160980. 99US-0160981. 99US-0160989. 99US-0161404. 99US-0161405. 99US-0161359. 99US-0161350. 99US-0161360. 99US-0161920. 99US-0161992. 99US-0161993. 99US-0154018. 99US-0154779. 99US-0160741. 99US-0160814. 99US-0160768 99US-0160770 23-AUG-1999; 25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 30-AUG-1999; 30-AUG-1999; 31-SEP-1999; 113-SEP-1999; 115-SEP-1999; 125-SEP-1999; 22-SEP-1999; 24-SEP-1999; 28-SEP-1999; 28-SEP-1999; 28-SEP-1999; 64-OCT-1999; 66-OCT-1999; 07-0CT-1999; 08-0CT-1999; 12-0CT-1999; 13-0CT-1999; 13-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 18-0CT-1999; 21-0CT-1999; 21-0CT-1999; 25-OCT-1999; 25-OCT-1999; 26-OCT-1999; 26-OCT-1999; 26-OCT-1999; 28-OCT-1999;

23;

Gaps

156; Indels 135;

|::| ::||: --RQLIPEVDHSAGIHSFPLLVLQVT 138

201

FIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKA¢RNDPFTEEEMTAMNLDRKTIVPYLEN

FFKCGGASLGVGMQHHAADGFSGLHFINTWSDMAR

GID---

85 VVKDLRDD--PSAPTIEGMRKAGYPMAMFDENIJAPRKTLPIGPGTGPDDPKPVILLQLN 142

102

143 139

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8

36 PTIVSTF--BOGLKR-FSEA-VPW--VAGQVKARG----ISEGNTGTSFIVPFEDVPRV

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                                                      ELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDA----RPA 298
                                                                                                             GEIANESLGATASRLRSELDPASM 343
                                                                                                                                        --- 343
  --- DVAGGDAVLTPVSASWAFFTFSPKAMS 242
                  The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                     237 ALK--AKSKEDGNTVSYSSYEMLAGHVWRSVGKAR--GLPNDQETKLYIATDGRSRLRPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                 344 RORTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRP
                                                                                                                             : : : : : | | | | | | LP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGGIHDFLVRMDDNYLRSALD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
7.3%; Score 169.5; DB 23; Length 433;
Best Local Similarity 23.0%; Pred. No. 6e-07;
Matches 105; Conservative 61; Mismatches 156; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; SEQ ID NO 2960; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                       434
                                                                                                                                                                                                                     IFE-----PVESLMYFMPKKP-DGEFCAALSLRDEDM
                                                                                                                                                                                                                                                                                                                                                                                                    Herbicidally active polypeptide SEQ ID NO 2960.
                                                                                                                                                                                                                                                                                                                                                                                                                                Herbicidal; plant; agriculture; herbicide.
                                                                                                           MGVSNNYPGLLQNMTYHNSTI-----
                                                                                                                                                                                                                                                                                                                    ABB93749 standard; Protein; 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-2001; 2001WO-EP09892.
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YTIGPEVDHQIVKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-269010/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FARE ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis
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PIIVSTF--EQGLKR-FSEA-VPW--VAGQVKAEG-----ISEGNTGTSFIVPFEDVPRV

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--NL---ROLIPEVDHSAGIHSFPLLVLQVT 138
44 PIGASNFFDEQVMKEALSKALVPFYPMAGRIKRDDDGRIEIDCNGAGVLFVV--ADTPSV 101
                                                                                                                                                                                                                                             GEIANESLGATASRLRSELDPASM 343
                                                                                                                                                                                                                                                                                              344 RORTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKRPETVRRP 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                        VVKDLRDD--PSAPTIEGMRKAGYPMAMFDENIIAPRKTLPIGPGTGPDDPKPVILLQLN
                                                                                        143 FIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMNLDRKTIVPYLEN
                                                                                                                                          --- DVAGGDAVLTPVSASWAFFTFSPKAMS
                                                                                                                                                                                           243 ELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDA----RPA
                                                                                                                                                                                                                                                           : | | | : : : | | | LP-----PGYFGNVIFTATPLAVAGDLLSKPTWYAAGQIHDFLVRMDDNYLRSALD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 61175.
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99US-0132048.
99US-0132407.
99US-0132484.
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99US-0127462
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99US-0129845
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                                                               102 I-----DDFGDFAPTL-
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09-MAR-1999
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US-0132486 US-0132687 US-0132687 US-0134218 US-0134218 US-0134221 US-0134387 US-0134387 US-0134981 US-0135214 US-0135629 US-0135629 US-0135629 US-0135629 US-0135629 US-0135629	990S-0137222. 990S-0137528. 990S-0137724. 990S-0138094. 990S-0138847. 990S-0139452. 990S-0139452. 990S-0139453. 990S-0139453. 990S-0139454. 990S-0139456. 990S-0139456.	US-0139767 US-0139767 US-0139817 US-0140355 US-014035 US-014099 US-0141287 US-0141287 US-0142305 US-0142305 US-0142305 US-0142305 US-0142305 US-0142305	10%-014408; 10%-014408; 10%-014408; 10%-014408; 10%-014433; 10%-014433; 10%-014433; 10%-014433; 10%-014433; 10%-014433; 10%-014433; 10%-014438; 10%-014438; 10%-014508; 10%-01
- MAY - 1999 - MAY - 1999	03 - CUN - 1999; 04 - CUN - 1999; 06 - CUN - 1999; 10 - CUN - 1999; 10 - CUN - 1999; 11 - CUN - 1999; 12 - CUN - 1999; 13 - CUN - 1999; 14 - CUN - 1999; 18 - CUN - 1999;	2004-1999 1004-1999	4 - 0 0 - 199 6 - 0 0 - 199 6 - 0 0 - 199 9 - 0 0 - 199 9 - 0 0 - 199 9 - 0 0 - 199 9 - 0 0 - 199 9 - 0 0 - 199 9 - 0 0 - 199 0 - 0 0 0 - 199 1 - 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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RR 23-7UL-1999; 99US-0145182.

RR 23-7UL-1999; 99US-0145218.

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RR 23-7UL-1999; 99US-0145218.

RR 23-7UL-1999; 99US-0145218.

RR 24-7UL-1999; 99US-0145218.

RR 24-7UL-1999; 99US-0145218.

RR 24-7UL-1999; 99US-0145919.

RR 22-7UL-1999; 99US-0145919.

RR 24-7UL-1999; 99US-0145919.

RR 02-AUG-1999; 99US-0145919.

RR 02-AUG-1999; 99US-0147302.

RR 03-AUG-1999; 99US-0147303.

RR 03-AUG-1999; 99US-0147302.

RR 13-AUG-1999; 99US-0147303.

RR 23-AUG-1999; 99US-0147303.

RR 23-AUG-1999; 99US-014733.

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RR 23-AUG-1999; 99US-014592.

RR 23-AUG-1999; 99US-014502.

RR 23-AUG-1999; 99US-014502.

RR 23-AUG-1999; 99US-014502.

RR 23-AUG-1999; 99US-015130.

RR 23-AUG-1999; 99US-015130.

RR 23-AUG-1999; 99US-015130.

RR 23-AUG-1999; 99US-01530.

RR 23-AUG-1999; 99US-01530.

RR 23-AUG-1999; 99US-01530.

RR 23-AUG-1999; 99US-015508.

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19-FEB-2002; 2002US-0078929.
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THORPE C J.
SAKAI H.
WENG Z.
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Sakai H,
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ODELL J T.
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                                     07-MAY-1999;
11-MAY-1999;
                                                              11-MAY-1999;
                                                      11-MAY-1999
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Thorpe CJ,
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(ODEL/)
(RAFA/)
(THOR/)
(SAKA/)
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(MEYE/)
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                                                                                                                                                                                          85 VVKDLRDD--PSAPTIEGMRKAGYPWAMFDENIIAPRKTLPIGPGTGPDDPKPVILLQLN 142
                                                                                                                                                                                                                             |: :| |: :| |: ---RQLIPEVDHSAGIHSFPLLVLQVT 154
                                                                                                                                                                                                                                                                                       --- DVAGGDAVLTPVSASWAFFTFSPKAMS 242
                                                                                                                                                                                                                                                                                                                                   253 ALK--AKSKEDGNTVSYSSYEMLAGHVWRSVGKAR--GLPNDQETKLYIATDGRSRLRPQ 308
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                                                                                                                                                                                                                                                                                                                         ELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDA----RPA 298
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                                                                                                                                                                              36 PIIVSTF--EOGLKR-FSEA-VPW--VAGOVKAEG----ISEGNIGISFIVPFEDVPRV
                                                                                                                                                                                                                                                                      RQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRP
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant; EST; expressed sequence tag; stress response; drought; heat; radiation; pathogen attack; grain flavour; disease resistance; peptide-methionine sulphoxide reductase; DNA repair; enzyme; intracellular protein transport.
                                                                                                                                                             Indels 135;
                                                                                                                                         7.3%; Score 169.5; DB 21; Length 449; 23.0%; Pred. No. 6.4e-07; ive 61; Mismatches 156; Indels 135;
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                                                                                                                                                                                                                                                                    FFKCGGASLGVGMQHHAADGFSGLHFINTWSDMAR
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                                                                                                                                                                                                                                                                                                                                                            MGVSNNYPGLLQNMTYHNSTI-
99US-0160814.
99US-01609815.
99US-0160981.
99US-0160981.
99US-0161404.
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99US-0161359.
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                     202 YTIGPEVDHQIVKA-
                                                                                                                                                    Similarity
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                                 22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
        21-OCT-1999;
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22-OCT-1999;
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26-OCT-1999;
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Matches 105;
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                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide-methionine sulfoxide reductase and nucleic acids, useful in improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           manipulating intracellular protein transport, and improving/protecting grain flavour. The nucleic acids may also be used as probes or amplification primers in the detection, quantitation or isolation of getranscripts, for recombinant expression of encoded polypeptides, as immunogens in preparing or screening antibodies, and in sense or antisense suppression of one or more genes in a host cell, tissue or plant. The proteins may be used as immunogens or antigens to obtain
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Weng Z;
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99US-133042P.
99US-133427P.
99US-133428P.
                                                                                                                                                           11-MAY-1999; 99US-133437P.
11-MAY-1999; 99US-133438P.
04-JUN-1999; 99US-137667P.
05-MAY-2000; 2000US-0566394.
                                                                                                                      99US-133436P.
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249
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ILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMNLDRKTI 195
                                                         SELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMGV
                                                                                                                                 SNNYP----GLLONMTYHNSTIGEIANESLGAT--ASRLRSELDPASMRORTRGLATYLH
                                                                                                                                              ---QPPLPEGYFGNVIFTATPLANAGTVTAGVAEGASVIQAALDRMD-DGYCRSALDYLE
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                                                                                                                                                                                               ------RPVFMGPGGIAYEG
                                            --PEVDHQIVKADVA-GGDAVLTPVSA----SWAFFTFSPKAM
                                                                                                           250 VRİR-SQVPAREGAPRF-STYAVLAAHVWRCASLAR--GLPADQPTKLYCATDGRQRL--
                                                                                                                                                                                                                                                                                                                                                                                  Plant, EST; expressed sequence tag; stress response; drought; heat; radiation; pathogen attack; grain flavour; disease resistance; peptide-methionine sulphoxide reductase; DNA repair; enzyme;
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               143 LVLQVTHFKCGGVAIGVGMQHHVADGFSGLHFINSWADLCRGVPI-
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LAFVLPSANRDGSLSVAISLQAEHMEKFR 440
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                                                                                                                                                                                                                                                                                              ABU58177 standard; Protein; 439
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ODELL J T.
RAFALSKI J A.
THORPE C J.
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Sakai H,
                                             VPYLENYTIG-
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FAMODU O O.
MEYERS B C.
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WENG Z.
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05-MAY-2000;
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Thorpe CJ,
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11-MAY-1999
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(SAKA/)
(WENG/)
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(ODEL/)
(RAFA/)
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The invention relates to isolated nucleic acids encoding plant stress response proteins (including peptide-methionine sulphoxide reductases) appearing as ABUS8148-ABUS8246 (or a protein 80% identical to them) from Zea mays, Oryza saltva, Glycine max, or Triticum aestivum. Also included are expression casettes, transformed host cells, transgenic plants/seeds, modulating the level of peptide-methionine sulphoxide reductase in a plant and a computer system/data processing system for identifying, analysing, or modelling a genetic sequence. The plant modelec acid is useful in developing strategies to improve plant response to stress (e.g. drought, heat, radiation or pathogen attack), engineering plants with increased disease and stress resistance, manipulating DNA repair and recombination efficiency, manipulating DNA repair and recombination of ficiency, manipulating DNA repair and recombination of ficiency manipulating DNA repair may also be used as probes or transcripts, for recombinant expression of encoded polypeptides, as immunogens in preparing or screening antibodies, and in sense or immunogens in sense or antipone transcripts of the plant may be used a simman protein or isolation of immunogens in preparing or some more genes in a host cell, tissue or immunogens in a host cell, thissue or immunogens in a host cell, thissue or immunogens in a more communication or income a minimal antibodies, and in sense or immunogens in a more communication or income a minimal antibodies, and in sense or an immunogens in a more communication or income a minimal antibodies.
                 New peptide-methionine sulfoxide reductase and nucleic acids, useful in improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor
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439 AA; Sequence

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                                                                                        TOISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVEWVAGQVKAEGISEGNTGTSFIVPFED
                                                                                                                              SNVDLVVP---NFHTPSVYFYRPNGVSNFFDA-----KVMKEALSK-----VLVPFYP
                                                                                                                                                                             VPRVVVKDLRDDPSAPTI----EGMR--KAGYPMAMFDENIIAP----RKTLPIGPGTGP
                                                                                                                                                                                                                          ---MAARLRRDDDGRVEIYCDAQGVLFVEAETTAAIEDFGDFSPTLELRQLIPSVDYSAG
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                                                                                                                                                                                                                                                                                                                                                                                               231 WAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFC
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                                             Gaps
                                             86;
                                                                                                                                                                                                                                                                                                                     127 IHSYPLLVLOVTYFKCGGVSLGVGMQHHVADGASGLHFINAWSDVAR----
24; Length 439;
                            .06;
195; Indels
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6.9%; Score 161; DB
                     Best Local Similarity 21.9%; Fred. No. 3.9e Matches 99; Conservative 72; Mismatches
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  Query Match
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RESULT 15 ABB93641 H

397

ABB93641 standard; Protein; 442 AA.

Herbicidally active polypeptide SEQ ID NO 2852. Herbicidal; plant; agriculture; herbicide 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892. (first entry) Weidler M; Arabidopsis thaliana WPI; 2002-269010/31. (FARB) BAYER AG WO200210210-A2. 31-MAY-2002 07-FEB-2002 Tietjen K, ABB93641;

The invention relates to identifying target proteins (ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an B-value sequences by a factor of 3 than the B-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides. Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant Claim 5; SEQ ID NO 2852; 261pp + Sequence Listing, English.

442 AA; Sequence 6.7%; Score 156.5; DB 23; Length 442; 21.1%; Pred. No. 1e-05; Live 68; Mismatches 174; Indels 101; Gaps 18; 230 80 VNNHEDDTVSFYIDCDGLGAKFV--HAKAESITVNDVLQSHGSVPY-----FISKFF 129 | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | 62 AEG-----ISEGNTGTSFIVPFEDVPRVVVKD-LRDDPSAPTIEGMRKAGYPMAMF 111 SKACRN--DPFTE----EEMTAMNLDRKTIVPYLENYTI---GPEVDHQIVKADVAGGDA 222 223 VLTPVSASWAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERID 282 ------FELSKRNILDLKAKANNEIDTNDLKISSLQAVVAYLMLSI--IRHSGLN 277 283 GSAPTEFCRAVDARPAMG--VSNNYPGLLQNMTYHNSTIGEIANESLGATASRL----RS 336 DENIIAPRKTLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLL 171 337 ELDPA-----SMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLW 386 61 24 KIHL-TPHDLDLLYLFYPQRGLLFHKPDPENSIIPRLMASLSTALEIY---FPFAGRLVK 79 4 KIQLDTLGQLPGLLSIYTQISLLY--PVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK 92; Conservative Query Match Best Local Similarity 112 172 Best Loca Matches g a Пр qq g à g à 8 à δ ð

--SLIISSSPRFEVY 381 338 ETNESYEVFAKNWVRNVKRPKTSFGSRLANN-387 DYDFGLGLGKPETVR 401 ::|| | || | 382 EHDF--GWGKPIAAR g à

7, 2004, 23:40:47

Search completed: February Job time : 554 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 23:31:29; Search time 72 Seconds (without alignments) 265.031 Million cell updates/sec February Run on:

US-10-614-954-6

1 MAFKIQLDTLGQLPGLLSIY......BDMDRLKADKEWTKYAQYVG 451 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 seqs, 42310858 residues Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Segments 6 Apply		Sequence	56	62,	2.7	7 Seguence 17.	28 Sequence 28,	Sequence 6	Sequence 60,	Sequence 68.	Sequence 73.	Seguence 6	Sequence 22.	Seguence 6	Sequence 67.	Sequence 34,	Sequence 45,	Sequence 54,	Sequence 20,	4 Sequence 7	Sequence 10.	equence 4,	7	2	Sequence 2, Appli	,
SUMMAKIES	e e	US-09-538-414-6	-414-	-09-538-414-	US-09-457-046B-	US-09-457-046B-6	US-08-207-904-2	7	US-09-457-046B-28	US-09-457-046B-69	US-09-457-046B-60	US-09-457-046B-68	US-09-457-046B-73	US-09-457-046B-66	US-09-457-046B-22	US-09-457-046B-63	US-09-457-046B-67	US-09-562-737-34	US-09-457-046B-45	US-09-457-046B-54	US-09-457-046B-20	US-09-457-046B-7	US-08-804-227C-1	US-08-804-198-4	US-08-854-585-2	US-09-447-533-2	PCT-US95-05512-2	US-09-457-046B-2
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	Length	451	459	474	448	436	448	448	439	451	435	439	445	433	306	482	450	830	440	441	303	446	3724	3724	1337	1337	1337	302
*	Query Match	100.0	79.7	41.2	6.1	6.1	5.7	5.7	5.7	5.6	5.4	5.4	5.3	5.5	5.2	5.2	5.1	5.0	4.8	4.8	4.6	4.5	4.5	4.5	4.5	4.5	4.5	4.5
	Score	2334	1860.5	962.5	142	141.5	134	134	132	130.5	126.5	125.5	124	122	21.	121.5	118	117	113	112	106.5	105.5	105.5	105.5	104.5		04.	104
	Result No.	1	7	E	4	S	ø	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Segmence 61. Appl	Sequence 4. Appli	4	70.	Sequence 72, Appl	٠,	Sequence 2, Appli	2.	2.	. 7	7	710			•	4	Sequence 4, Appli	4,
US-09-457-046B-61	US-09-147-236-4	US-09-522-474-4	US-09-457-046B-70	US-09-457-046B-72	US-08-542-003-2	US-08-322-760A-2	US-09-236-949-2	US-09-457-046B-2	US-08-981-690-2	US-09-455-777-2	US-09-328-352-7107	US-09-252-991A-30777	US-09-252-991A-16967	US-09-243-374-4	US-07-876-280-4	US-07-675-772-4	US-08-063-170-4
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458	802	802	461	455	1289	1289	1289	306	260	610	347	356	2482	446	1289	1289	1289
4.4	4.4	4.4	4.3	4.3	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1
103.5	102	102	100	99.5	99.5	99.5	99,5	66	98.5	98.5	97	97	6	95.5	95	95	95
28	53	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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                                                 Sequence (A Application US/09538414)

Patent No. 6346655

GENERAL INFORMATION:

APPLICANT: Hohn, T.

APPLICANT: Balmeron, J.

APPLICANT: Reinders, C.

APPLICANT: Reinders, J.

APPLICANT: Ringers, J.

APPLICANT: Reinders, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Fusarium graminearum
US-09-538-414-6
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Best Local Similarity 100.
Matches 451; Conservative
US-09-538-414-6
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61 KAEGISEGNIGISFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120

1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV

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1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV

61 KAEGISEGNIGISFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK

121 TLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180

121 TLPIGPGTGPDDPKPVILLQLNPIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF

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181 TEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA

241 MSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMG

181 TEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPKA

180 240 300

301 VSNNYPGLLQNMTYHNSTIGELANESLGATASRLRSELDPASMRQRTRGLATYLHNNPDK 360

241 MSELKDAATKTIDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMG 300

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US-09-538-414-8
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                                                                                                                                                                                                         SOFTWARE: I
                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                          Matches
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301 VSNNYPGLLQNMTYHNSTIGELANESLGATASRLRSELDPASMRQRTRGLATYLHNNPDK 360
                                                    420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 SNNYPGLLONMTYHNSTIGEIANESLGATASRLRSELDPASMRORTRGLATYLHNNPDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK
                           SIVOSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMPKKPD
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.7%; Score 1860.5; DB 4; Length 459; 77.6%; Pred. No. 1e-184; ive 50; Mismatches 50; Indels 1;
                                                                                                                                                                                                                                                           APPLICANT: Reinders, J.
APPLICANT: Ruznia, R.
APPLICANT: Kuznia, R.
APPLICANT: Kuznia, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist
CURRENT APPLICATION NOWBER: US/09/538,414
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
                                                                               421 GEFCAALSLRDEDMDRLKADKEWTKYAQYVG 451
                                                                                             421 GEFCAALSLRDEDMDRLKADKEWTKYAQYVG 451
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                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Fusarium sporotrichioides US-09-538-414-2
                                                                                                                                                                     Sequence 2, Application US/09538414
Patent No. 6346655
GENERAL INFORMATION:
APPLICANT: Hohn, T.
APPLICANT: Patents, C.
APPLICANT: Peters, C.
APPLICANT: Rendra, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.6%
Matches 349; Conservative
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 459
                                                                                                                                              RESULT 2
US-09-538-414-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPGTG-PDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEE 183
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF TIMENENCE: 35479
CURRENT APPLICATION UNBER: US/09/457,046B
CURRENT APPLICATION DATE: 1999-12-07
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 MGVSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRSELDPA--SMRQRTRGLATYLHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 GNTIGMAAKSGPVFAVQANFISGGLVLTIVGQHNIMDITGGESIINLLNKSCHQKPFSDE
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320 LGLPETYPGLLVNMTFNTGSLKSLDHKSLGVLASQIRRKLDPKVFDLAYNTCALATLLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 NPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDPGLGLGKPETVRRPIFEPVESLMYFMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 CPDKTKVSIPQPIDTLSGIMVSSWAKVSLYDVDFNLGLGKPKSVRRPRFISLESLIYFMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 EMTAMNLDRKTIVPYLENYTIGPEVD--HQIVKA--DVAGGDAVLTPVS-ASWAFFTFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 KAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 962.5; DB 4; Length Pred. No. 2.9e-91; B4; Mismatches 158; Indels
                                                                                                                      APPLICANT: Peters, C.
APPLICANT: Kendra, D.
APPLICANT: Reinders, D.
APPLICANT: Reinders, D.
APPLICANT: Reinders, R.
APPLICANT: Buill-MacKey, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/09/538,414
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-457-046B-56; Sequence 56, Application US/09457046B; Patent No. 6287835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Saccharomyces cerevisiae
Sequence 8, Application US/09538414
Patent No. 6346655
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.2%;
                                                                                                                                                                                                                                                                                                                                                                     PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202; Conservative
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Best Local Similarity
                                                                                                    APPLICANT: Salmeron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                         APPLICANT: Hohn, T
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360 KSNVSLTADADPSTSV------MLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVE 409
                                                                                                              333 KSSSRIFELLBEIGKVYGRGNEMDLWMSNSWCKLGLYDADF--GWGKPVWVTGRGTSHFK 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 RLELDCNASGIVLMEAETEAKLDDLGDF8PSP------DLNSLFPRVDYTI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 PIGPGTGPDDPKPVILLQL-NFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKA--CRNDP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DELPLIFVQLTKFQCGGIALSFAISHAVVD--GQSALYFLTEWASLARGEP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 FTEEEMTAMNLDRKTI-----VPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASW 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 TQISLLY------PVSDSSQYPTIVSTFEQGLKR-----FSEAVPWVAGQVKAEG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 THVPTIYYYRFCHDCLPSTDN-----IIKTLRTSLSKALVHFYPLSGRLRWIAG----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Anther-Specific CDNA Sequences, Genomic TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences NUMBER OF SEQUENCES: 21

NUMBER OF SEQUENCES: 21

ADDRESPONDENCE ADDRESS:
ADDRESSEE: CLEA-GEIGY Corporation
STREBET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Mismatches 183; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
                                                                                                                                                            410 SLMYFMPKKPDGEFCAA-LSLRDEDMDRLKADKE 442
                                                                                                                                                                                      DB 1;
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21.7%; Pred. No. 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/908,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       US-08-207-904-2; Sequence 2, Application US/08207904; Patent No. 5477002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Tuttle, AnnMarie
APPLICANT: Crossland, Lyle D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Lazar, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (919)541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-207-904-2
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USA
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STATE: Ne
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 KPLVEPVW-----BIRELIKPEDLMHLQFHKFG--LIRQPLKLD-----EICQAS 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 DARPAMGVSNNYPGLLQNMTYHNSTIG------EIANESLGATASRLRSELDPASMR 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---EEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPK 239
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                                                                                                                                                                                                      64
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Patent No. 6287835
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 622
                                                                                                                                                                                                                                                                                                                                                                                                      5 IQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEG
                                                                                                                                                                                                                             ------DAQNASYEQLLF-----
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                                                                                                                                                            Gaps
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                                                                                                            Length 448;
                                                                                                          ; Score 142; DB 3; Length 44; Pred. No. 5.9e-06; 61; Mismatches 184; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 KPLDELPSKPMDRK------EEVEE--
                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                          Query Match 6.1%;
Best Local Similarity 20.5%;
                                                                                                                                                      84; Conservative
                                         ORGANISM: Taxus cuspidata
                                                              US-09-457-046B-56
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LENGTH: 448
TYPE: PRT
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Db 84 RLELDCNASGIVLMEATERAKLDDIGDFSPSPDLNSLFPRVDYII 128 Qy 123 PIGPGTGPDDFKPVILLQL-NFIKGGILITTVNGQHGANDWVGQDAVIRLLSKACRNDP 179	276 HKFEQPTNLCICVNIRNIMQPPLPKSYFGNAIVDVIANGVSGDITSRPLEYVARRVR- 337 ELDPASNEQRIRGIATYLHNNPDKSNVSLTADADPSTSVMLSSW 338AAIRMVTSDYANSTIDFLKNQEDLSKYQDIHAFRSKEGPFYGNPNLGVISW 381 AKVGLWDYDFGLGKPFTVRRPIFEPVESLMYFMP-KKPDGEFCAALSLRDEDMDRLK 4 384 ISLPLLGLDFGWGKEIHMSPGTHEYDGDCVILPGKEGDGSLTVAIILQAVHVDAFK 4	RESULT 8 US-09-457-046B-28 Sequence 28, Application US/09457046B Sequence 28, Application US/09457046B Patent NO. 6287355 GENERAL INFORMATION: APPLICANT: Croteau, Rodney et al. TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway TITLE OF INVENTION: 1999-12-07 CURRENT FILING DATE: 1999-12-07 NUMBER OF SEQ ID NOS: 74 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 28 IENGTH: 439 TYPE: ATPE: TAXES Cuspidata US-09-457-046B-28	Query Mat Best Loca Matches	GPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLL ::	QY 226 PVSASWAFPTESPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSA 285
		VVENTION: SEQUENCES SECUENCES SECUENCES TO SEQUENCES TO S	9 18 8.1 9 18 18 18 18 18 18 18 18 18 18 18 18 18	Score 134;	Best Local Similarity 21.7%; Fred. No. 46-U5; Matches 104; Conservative 58; Mismatches 183; Indels 134; Gaps 24; Qy 21 TOISLIYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQYKAEG 64 Db 34 THVPTIYYYRFCHDCLBSTDNIIKTLRTSLSKALVHFYPLSGRLRWIAGS 83 Qy 65 ISEGNIGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPWAMFDENIIAPRKTL 122

435

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APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
SUFFRENT FILING DATE: 74
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 60
GENERAL INFORMATION:
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                             435
         340 PASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGCKPFFT 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 TDNVEERKKKKTIVVMLPLSTS-----QLQKLRSKANGSKHSDPAKGF-TRYETVTG 269
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.6%; Score 130.5; DB 3; Length 451; Best Local Similarity 21.7%; Pred. No. 9.4e-05; Matches 105; Conservative 64; Mismatches 195; Indels 119
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                                                                                 421
                                                                                                                ---PVQQQSALAMQNYFLFLKPSKNKPDG 409
                                                                             VRRPIFEPVESLM--YFM----PKKPDG
                                                                                                                                                                                                 Sequence 69, Application US/09457046B Patent No. 6287835 GENERAL INFORMATION:
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US-09-457-046B-69
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US-09-457-046B-60; Sequence 60, Application US/09457046B; Patent No. 6287835

RESULT 10

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                                                                                                                                                                                                                                                                                                                                                                                                                                      117 APRKTLP-IGPGTGPDDPKPVILLQLNFI--KGGLILTVNGQHGAMDMVGQDAVIRLLSK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 ACRNDPFTEEEMTAMNLDRKTIVPYLENYTIGPRVDHQIVKADVAGGDAVLTPVSASWAF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DWAT----TTAKGKSNSTI-EFAETTIYPPPPSHMYEQFPSTDSDSNIT---SKXVL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 QAMDIRLRIPSSVAPKDVIGNIQSGFSLKKDAESEFEI----PEIVATFRKNKERVNEMI 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 NESLGATASRIRSELDPASMRQRTRGLATYLHNNPDKSNVSLTAD-ADPSTSV---MLSS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SRVRLERIDGSAPTEFCRAVDARPAMGVSNNYPGLLQNMTYHNSTIGEIA 323
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Patent No. 6287835
GENERAL INPERMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 68
                                                                                                                                                                                                                                                      23 RLQLSILDLYCPG---IYVSTIFFYDLITESSE-----VFSENLKLSLSETLSRFYP-L
                                                                                                                                                                                                                       4 KIQLDTLG-QLPGLLSIYTQISLLYP-VSDSSQYPTIVSTFEOGLK-----RFSEAVPWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                         5.4%; Score 126.5; DB 3; Length 435; 20.2%; Pred. No. 0.00023; tive 77; Mismatches 182; Indels 133;
                                                                                                                                                                                                                                                                                                                                                                     234 --FIFSPKAMSELK-DAATKILDASTKFVSTDDALSAFIWKSA-
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-60
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i TYPE: BRT
i ORGANISM: Catharanthus roseus
US-09-457-0468-68
                                                                                                                                                              99; Conservative
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                                                                                                                                     Best Local Similarity
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US-09-457-046B-68
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                                                                                                           Query Match
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70 TGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENI-----IAPRKTL 122
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                                                                                                                                                                                                        ---LRSELDPASMRQRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDF 390
                                                                                                                                                                                                                                     346 DDYLRSAIDHTESKP---GLPVPYMG8PEKTLY------PNVLVNSWGRIPYQAMDF 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIGPG---TGPDDPKPVILLOLNFIK-GGLILITVNGQHGAMDMVGQDAVIRLLSKACRNDP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 ---ASRVRLERIDGSAPTEFCRAVDARPAMGVSNNYPGLLQNMTYHNSTIGEIANESLGA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 MNLRKRIKL-ALENDVSGNFFIVVNAESKITVAFKITDLTESL---GSACGEIISEVAKV 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 DDAEVVSSWVINSVRE-----FYYEWGKGEKNVFL-----YTSWCRFFLYEVD 377
                                                             17 LSIYTQISLLYPVSDSSQYPTI-----VSTFRQGLKRFSEAVPWVAGQVKAEGISEGN 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 66, Application US/09457046B
Patent No. 6287835
GENERAL INFORMATION:
APPLICANT Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway FILE REFERENCE: 53679
CURRENT PPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 LVGLSGFLSETETPPLAAIQLNMFKCGGLVIGAQFNHIIGDMFTMSTFMNSWAKACR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 FTEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPK
                                     SASWAFFTFSPKAMSELKDAATKTLDAS--TKFVSTDDALSAFIWKSASRVRLERIDGSA
                                                                                                                                                                                                                                                                                           391 GLGLGKPETVRRPIFEPVESLMY-----FMPKKP-DGEFCAALSLRDEDMDRLK 438
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L Similarity 20.3%; Pred. No. 0.00067;
97; Conservative 64; Mismatches 196; Indels 122;
                                                                                                                        286 PIEFCRAVDARPAM---GVSNNYPGLLQNWTYHNSTIGEIANESLGATASR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 LSLLDQIQIPFYVGLIFHYETLSDNSDITLSKLRSSLSETLTLYYHVAGRY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 433;
DRYLHLRPRNPP----QIKYSHSQFEPFVPSLPNELLDGK--
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US-09-457-046B-66
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Best Local S:
Matches 97
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                                             23;
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                                                                                                                                                                        133
                                                                                                                                                                                                                                                         134 KPVILLQINFIKGGLILTVNGQHGAMDMVGQDAVIRLLSK----ACRNDPFTEEEMTAM 188
                                                                                                                                                                                                                                                                                     189 NIDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWA--FFTFSPKAMSELKD 246
                                                                                                                                                                                                                                                                                                                                                                                                                          247 AATKTLDASTKFVSTDDALSAFIWKSA----SRVRLERIDGSAPTEFCRAVDARPAMGV 301
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APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 73
                                                                                                                            39 NIYQTCVSVGFFYENPDGIEISTIREQLQNSLSKTLVSYYPFAGKVVKNDYIHCNDDGIE
                                                                                                                                                                      FIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRKTLPIGPGTGPDDP
                                                                                                                                                                                                               ---LKYELRSYARDLVLPKRVT----VGSEDT
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                                                                                       18 SIY---TQISLLYPVSDSSQYPTIVSTFEQGL-KRFSEAVPWVAGQVKAEGISEGNTGTS
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                                             Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 YTQISLLYPVSDSSQ---YPTIVSTFEQG--LKRFSEA-VPW--VAGQVKAEG
        Length 439;
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    Query Match 5.4%; Score 125.5; DB 3; Best Local Similarity 20.5%; Pred. No. 0.0003; Matches 95; Conservative 75; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 73, Application US/09457046B
Patent No. 6287835
                                                                                                                                                                                                             99 FV---EVRIRCRMNDI-----
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                                                 GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 53679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPERBRUCE: 35679
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                135 PVILLOLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEEMTAMNLDRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 IVPYLENY-----TIGPEVDHQIVKADVAGGDAV-----LIPVSASAWAFFIFSPKAMSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KPPK--IVHINNLIPCNIIAMAGSPRFPIYNNDFGWG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 GLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
                                                                                                                                                                                                                                                                                                                                               5.2%; Score 121.5; DB 3; Length 3 20.7%; Pred. No. 0.00042; ative 44; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLLAVOATKLKDGIALAITVNHAVADATSVWHFISSWAQLCK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 SNNYPGLLQNMTYHNSTIGEIANESLGATA----
                   Sequence 22, Application US/09457046B Patent No. 6287835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 63, Application US/09457046B Patent No. 6287835 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Arabidopsis thaliana US-09-457-0468-63
                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                   ORGANISM: Taxus cuspidata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-457-046B-63
US-09-457-046B-22
                                                                                                                                                                                                                                                                                                         US-09-457-046B-22
                                                                                                                                                                                                                       SEQ ID NO 22
LENGIH: 306
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112 DENIIAPRKTTPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLL 171
                                                                                            172 SKACRNDPFTEEEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASW 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 RERIFSFSRESIQELKAVVNKKKWLIVDNGEIDGVELLGKQSNDKLNGKENGILTEMLES 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 KSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKFETVRRPIFEPVESLMYFMP-KK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DASTKFVSTD----DALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMGVSN
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Search completed: February 7, 2004, 23:48:38 Job time: 73 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

7, 2004, 23:46:34; Search time 249 Seconds (without alignments) 379.243 Million cell updates/sec February Run on:

US-10-614-954-6 2334 Perfect score: Title:

1 MAFKIQLDTLGQLPGLLSIY.....BDMDRLKADKEWTKYAQYVG 451 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Total number of hits satisfying chosen parameters:

801455 segs, 209382283 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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/cgn2_6/ptcodata/1/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Reg

Description	Sequence 6. Appli		œ	64	Sequence 52, Appl	. 09	200	56.	26	26	26	62	22	2	Sequence 62, Appl
ID	US-10-074-279-6	US-10-074-279-2	US-10-074-279-8	US-10-078-929-64	US-10-078-929-52	US-10-078-929-60	US-10-078-929-200	US-09-866-572A-56	US-09-866-570A-56	US-10-166-984-56	US-10-166-984-56	US-09-866-572A-62	US-09-866-570A-62	US-10-166-984-62	US-10-166-984-62
DB	14	14	14	14	14	14	14	10	10	12	15	10	10	12	15
Query Match Length DB	451	459	474	436	446	439	431	448	448	448	448	436	436	436	436
Query Match	100.0	79.7	41.2	7.3	7.2	6.9	6.2	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1
Score	2334	1860.5	962.5	170.5	168.5	161	144	142	142	142	142	141.5	141.5	141.5	141.5
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	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl							
	28,	28,	28,	28,	. 69	.69	69	69	.09	60,	75.	75.	.89	68,	68	68,	73	73	73,	73,	.99	.99	.99	.99	22,	22,	22,	22,	63,	63,
	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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	9-866-572A-28	570A-28	984-2	984-28	572A-69	570A-69	984-69	984-69	572A-	570A-60	984-75	0-166-984-75	572A-68	570A-68	166-984-68	984-68	572A-73	570A-73	984-73	984-73	572A-66	570A-66	984-66	984-66	572A-22	570A-22	984-22	984-22	572A-63	570A-63
	-998		-991	166-	-998	-998	1-166-5	166-	-998	-998	166-9	-991	-998	-998	166-	0-166-	-998	-998	-991	-991	-998	-998	166-	166-	-998	-998	166-	166-	-998	-998
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,	10	10	12	15	10	10	12	15	10	10	12	15	10	10	12	15	10	10	12	15	10	10	12	15	10	10	12	15	10	10
	439	439	439	439	451	451	451	451	435	435	435	435	439	439	439	439	445	445	445	445	433	433	433	433	306	306	306	306	482	482
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٠	16												28				32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
APPLICANT: Dill-Mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods:
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/10/074,279
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: US/09/538,414
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
                Sequence 6, Application US/10074279
Publication No. US20020162136A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Fusarium graminearum
US-10-074-279-6
                                                                                                                                                           Reinders, J.
Kuznia, R.
Dill-Mackey, R.
                                                                                               Salmeron, J.
Peters, C.
Kendra, D.
US-10-074-279-6
                                                                                                 APPLICANT:
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APPLICANT:
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APPLICANT:
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1 MAFKIQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV Gaps ö Length 451; Indels 100.0%; Score 2334; DB 14; 100.0%; Pred. No. 3.7e-222; iive 0; Mismatches 0; 1 Query Match Best Local Similarity 100. Matches 451; Conservative à

0

61 KAEGISEGNIGISFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120 61 KAEGISEGNTGTSFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPRK 120 9 1 MAFKIQLDTLGQLPGLLSIXTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWAGGV g à

421

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SEGNICISFIVPFEDVPRVVVKDLRDDPSAPTIRGMRKAGYPMAMFDENIIAPRKTL-PI 124
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250 SELKDAATKTLDASSKFVSTDDALSAFIWQSTSRWRLARLDASTPTEFCRAVDMRGPMGV 309
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320 IGLPETYPGILVNMTFNTGSLKSLDHKSLGVLAŞQIRRKLDPKVFDLAYNTCALATLLSR
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                                                                                                          362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFEPVESLMYFMPKKPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 QLDILGQQPSLYKLYTQICSIYRVPDPSAHDHIVNTLTRGLETLAKNFQWLAGNVVNBGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPGTG-PDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEE
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                                                    310 SSTYPGILONMTYHDSTVAEIANEPLGATASRIRBEINSDRIRRRTQALATYMHGLPDKS
                                  302 SINYPGILIONMTYHNSTIGEIANESLGATASRIRBEIDPASMRORTRGLATYLHINNPDKS
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41.2%; Score 962.5; DB 14; Length
Best Local Similarity 44.4%; Pred. No. 2.9e-86;
Matches 202; Conservative 84; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hohn, T.
APPLICANT: Salmeron, J.
APPLICANT: Beters, C.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Rinders, J.
APPLICANT: NUMBER: US/10/074,279
CURRENT APPLICATION NUMBER: US/10/074,279
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                       430 EFTASISLRDEDMERLKADEEWTKYAKYIG 459
                                                                                                                                                                                       EFCAALSLRDEDMDRLKADKEWTKYAQYVG 451
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; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-8
                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/10074279; Publication No. US20020162136A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 8
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                              TLPIGEGTGEDDFKPVILLQLNFIKGGLILTVNGQHGAMDWVGQDAVIRLLSKACRNDPF
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       TLPIGPGTGPDDPKPVILLQLNFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF
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Publication No. US20020162136A1

GENERAL INFORMATION:

APPLICANT: Boln, T.

APPLICANT: Reinfar, C.

APPLICANT: Reinfar, D.

APPLICANT: Reinfars, D.

APPLICANT: Ruznia, R.

CURRENT FILING DATE: 2002-02-12

FRICH FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                   GEFCAALSLRDEDMDRLKADKEWTKYAQYVG 451
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Matches 349; Conservative
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SOFTWARE: Patentin Ver. 2
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Publication No. US20020152497A1
GENERAL INFORMATION:
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Falco, Saverio Carl
Sakai, Hajime
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Odell, Joan T.
Meyers, Blake
Thorpe, Catherine
Weng, Zude
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APPLICANT: Miao, Guo-Hua
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Best Local Similarity 20.4%; Pred. No. 7.3e-08;
Matches 84; Conservative 61; Mismatches 158; Indels 109; Gaps
                                                                417 KKPDGEFCAALSLRDEDMDRLKADKEWTKYAQYVG 451
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PRIOR APPLICATION NUMBER: 60/133038
PRIOR PILING DATE: 1299-05-07
PRIOR PILING DATE: 1299-05-07
PRIOR PILING DATE: 1299-05-07
PRIOR PILING DATE: 1299-05-07
PRIOR PILING DATE: 1399-05-11
PRIOR APPLICATION NUMBER: 60/133427
PRIOR PILING DATE: 1399-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR PILING DATE: 1399-05-11
PRIOR PELING DATE: 1999-05-11
PRIOR PAPLICATION NUMBER: 60/133438
PRIOR PILING DATE: 1999-05-11
PRIOR PAPLICATION NUMBER: 60/133438
PRIOR PILING DATE: 1999-05-11
PRIOR PAPLICATION NUMBER: 60/133436
PRIOR PILING DATE: 1999-05-11
PRIOR PAPLICATION NUMBER: 60/133436
PRIOR PILING DATE: 1999-05-11
PRIOR PAPLICATION NUMBER: 60/13346
PRIOR PILING DATE: 1999-05-11
PRIOR PAPLICATION NUMBER: 60/137667
PRIOR PILING DATE: 1999-06-04
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Publication No. US20020152497A1
GENERAL INFORMATION:
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APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
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SOFTWARE: Microsoft Office 97
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--NIIAP----RKTLPIGPGTGPDDPKPV 136
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                               Indels 111;
                    384 GLWDYDFGLGLGKPETVRRPIFEPVESLMYFMPKKPDGEFCAALSLRDEDMD
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21.8%; Pred. No. 1.2e-07;
tive 63; Mismatches 177;
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GGDAVLTPVSAS 230

---RPIFMGP 396

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231 WAFFIFSPKAMSELKDAATKILDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFC 290
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                                                                                                  DDPKPVILLQLNFIK-GGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPFTEEMTAMN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 RAVDARPAM--GVSNNYPGLLQNMTYHNSTIGEIANESLGATASRLRSELDPASMRQRTR
                                                                                                                                                                     127 IHSYPLLVLOVTYFKCGGVSLGVGMOHHVADGASGLHFINAWSDVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 GGIAYEGLSFIIPSSTNDGSLSLAIALPPEQM 428
                                                                                                                                                                                                                                           190 LDRKIIVPYLENYTIG-----PEVDHQIVKADVA
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PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR PRIOR DATE: 1999-05-11
PRIOR PRILING DATE: 1999-05-11
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PRIOR PRILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR PRILING DATE: 1999-05-11
PRIOR PRILING DATE: 1999-05-11
PRIOR PRILING DATE: 1999-05-11
PRIOR PRILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: MICROSOFT OFFICE 97
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PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
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Falco, Saverio Carl
Sakai, Hajime
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Odell, Joan T.
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Thorpe, Catherine
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; ORGANISM: Ipomoea batatas
US-10-078-929-200
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Thorpe, cc.
Zude
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                                                                                                                                                                                                                  302 SNNYP----GLLQNMTYHNSTIGEIANESLGAT--ASRLRSELDPASMRQRTRGLATYLH 355
                                                                                                                                                                                                                                                                304 ---QPPLPEGYFGNVIFTATPLANAGTVTAGVAEGASVIQAALDRMD-DGYCRSALDYLB 359
                                                                                                                                                                                                                                                                                                                                                                                                                       ---RPVFMGPGGIAYEG 411
          190 MPFIDRSLLRARDPPTPAYPHIEYQPAPAMLSEPPQAALTSKPATPPTAVAIFKLSRAEL 249
                                                                                242 SELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFCRAVDARPAMGV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
FILE REFERENCE: BB1357 US NA
CURRENT PELLON NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
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                                                                                                                           356 NNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRPIFE-----PVES
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21.9%; Pred. No. 6.5e-07;
cive 72; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                               360 LQPDLSALVRGAHTFRCPNLGLTSWVRLFIHDADFGWG-
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PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
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PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60, Application US/10078929
Publication No. US20020152497A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/133038
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PRIOR FILING DATE: 1999-05-11
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PRIOR APPLICATION NUMBER: 60/133438
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Falco, Saverio Carl
Sakai, Hajime
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Odell, Joan T.
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NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
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Thorpe, Catherine
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; ORGANISM: Glycine max
US-10-078-929-60
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Best Local Similarity
Matches 99; Conserv
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APPLICANT:
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Sequence 56, Application US/10166984
Publication No. US20040005562A9
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Taxus cuspidata
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344 LRSRIVA-
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US-10-166-984-56
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                                                                                                                                                                                                                                         228 TTMLKITPEQLALIK---TKSKHEG----STYELLAAHIWRCACKAR--GLIDDQATKLY 278
                                                                                                                                                                                                                                                                                                                                                                  403
                                                                                                                                                                    180 LSVAIPPFIDRTLIAA---RDPPTPAFEHSEYDQPPKL--KSVPESKRGS-----SAS 227
                                                                                                                                                                                                                  WAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSAFIWKSASRVRLERIDGSAPTEFC 290
                                                                                                                                                                                                                                                                                       291 RAVDAR----PAMGVSNNYPGLLQNWTYHNSTI----GEIANESLGATASRLRSELDPASM 343
                                                                                                                                                                                                                                                                                                                               332
                                                                                                                                                                                                                                                                                                                                                                                   333 DEYLRSALDFLECQPDLSKLIRGSNYFASPNLNINSWTRLPVHESDFGWG-----RP 384
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                                                                                                      RKFIPTVDTSGDISSFPLIIFQVTRFKCGGVCLGTGVFHTLSDGVSSLHFINTWSDMARG 179
                                                                                                                                           -----DPFTEEEMTAMNLDRKTIVPYLEN--YTIGPEVDHQIVKADVAGGDAVLTPVSAS 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 -SLP--PNIQVQDLHPLILQVTRFTCGGFVVGVGFHHGICDARGGTQFLQGLADMARGET 193
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION NUMBER: US/09/866,572A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/457,046
PRIOR FILING DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                           279 VATDGRSRLCPPLP----PGYLGNVVFTATPMAESGELQSEPLTNSAKRIHSALSRMD-
                                                                                                                                                                                                                                                                                                                                                              344 RORTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGLGKPETVRRP
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                                       Gaps
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   DB 14; Length 431;
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   ; Score 144; DB 14; Length 4; Pred. No. 3e-05; 48; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   404 I-FEPV----ESLMYFMPK-KPDGEFCAALSLRDEDMDRLK 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 KPLVEPVW----NRELIKPEDLMHLQFHKFG--LIRQPLKLD
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6.2%;
illarity 24.6%;
Conservative 48
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Best Local Similarity 20.5*
Matches 84; Conservative
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SOFTWARE: PatentIn Ver. 2.1
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                Similarity
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US-09-866-572A-56
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                                 84;
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LENGTH: 448
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 Query Match
Best Local
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DARPAMGVSNNYPGLLQNMTYHNSTIG-----EIANESLGATASRLRSELDPASMR 344
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Patent No. US20020168745A1

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway

TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway

CURRENT PPLICATION NUMBER: US/09/866,570A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US/09/457,046B

PRIOR FILING DATE: 1999-12-07
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION TRANSACYLAST
CURRENT APPLICATION NUMBER: US/10/166,984

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: US 09/866,570
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                                                                                                                                                                                           345 QRTRGLATYLHNNPDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 ISE-----GNTGTSFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAMFDENIIAPR 119
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ITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 4630-62267
CURRENT APPLICATION NUMBER: US/10/166,984
CURRENT FILING DATE: 2002-06-10
PRIOR PILING DATE: 2001-06-15
PRIOR FILING DATE: 1201-06-15
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 20.5%; Pred. No. 5.1e-05;
Matches 84; Conservative 61; Mismatches 184;
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/457,046
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PATCHIN VEY: 2.1
SEQ ID NO 56
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CRGANISM: Taxus cuspidata
US-10-166-984-56
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ORGANISM: Taxus cuspidata
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Patent No. US20020138859A1
GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REFERENCE: 55679
CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/457,046
PRIOR APPLICATION NUMBER: 09/457,046
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5 IQLDTLGQLPGLLSIYTQISLLYPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEG
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Sequence 62, Application US/10166984

Sequence 62, Application US/10166984

Publication No. US20040005562A9

GENERAL INFORMATION:
TITLE REPERENCE: 4630-62267

TITLE REFERENCE: 4630-62267

CURRENT APPLICATION NUMBER: US/10/166,984

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2001-05-25

PRIOR RELING DATE: 1999-10-07

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1999-10-07

PRIOR FILING DATE: 1999-10-30

NUMBER OF SEQ ID NOS: 76

SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                  ; Sequence 62, Application US/09866570A

; Patent No. US20020168745A1

; GENERAL INFORMATION:

APPLICANT: Croteau, Rodney et al.

; ATILE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
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                                391 NLMLLIDTK-DGEGIEAWITLTEEQMSLFECDQE 423
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         410 SLMYFMPKKPDGEFCAA-LSLRDEDMDRLKADKE
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CURRENT APPLICATION NUMBER: US/09/866,570A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US/09/457,046B

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 74

SOFTWARE: Patentin Ver, 2.1
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183 ---EEMTAMNLDRKTIVPYLENYTIGPEVDHQIVKADVAGGDAVLTPVSASWAFFTFSPK 239
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
FILE REPERENCE: 4630-62267
CURRENT APPLICATION NUMBER: US/10/166,984
CURRENT FILING DATE: 2002-06-10
PRIOR PELICATION NUMBER: US 09/866,570
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/457,046
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
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                                                                                                                Query Match 6.1%; Score 141.5; DB 12; Length Best Local Similarity 22.2%; Pred. No. 5.5e-05; Matches 74; Conservative 56; Mismatches 133; Indels
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TYPE: PRT ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Db	227	227 KIKKLRAKASRNLVKNPTRVEAVTALFWRCVTKVSRLSSLTPRTSVLQILV 277
λo	300	300 GVSNNYPGLLQNMTYHNSTIGETANESLGATASRLRSELDPASMRQRTRGLATYLHNNPD 359
Ωp	278	NIRGKVDSI.CENTIGNMI.SIMILKNEEAAIERIQDVVDBIRRAKEIFSINCKEMS 332
à	360	360 KSNVSLTADADPSTSVMLSSWAKVGLMDYDFGLGLGKPETVRRPIFEPVE 409
qq	333	333 KSSSRIFELLEEIGKVYGRGNEMDLMMSNSWCKLGLYDADFGWGKPVWVTGRGTSHFK 390
δλ	410	410 SIMYEMPKKPDGEFCAA-LSIRDEDWDRLKADKE 442
qu	391	391 WLMLLIDTK-DGEGIEAWITLTEEQMSLFECDQE 423
Search completed: For Job time : 249 secs	mplet : 24	Search completed: February 8, 2004, 00:12:21 Job time : 249 secs

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Wing, R., Menblauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen Wing, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main
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                                                                                                                                                   661 GACGCTGT-TCTCACGCCGGTCAGTGCAAGCTGGGCGTTCTTCACATTCAGCCCCAAGGC
ACGTTACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGCCTGTAATTCTATTGCAG
                                    470 ACGITACCIATIGGACCIGGTACIGGICCCGACGACCCAAGCCIGIAATICIATIGGAG
                                                                                                                                                                                                                 481 ATGGTAGGCCAAGATGCGGTGATCCGTCTACTCTCCAAGGCGTGCCGTAACGACCCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                        601 AACTATACGATTGGCCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGT
                                                                                                           CTCAACTTCATCAAGGGGGGACTCATCCTCACTGTCAAGGGACAGCACGGTGCTATGGAT
                                                                                                                                                                                                                                                                                                                            541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA
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/mol_type="mRNA"
/cultivar="Morex"
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100 Jordan Hall, Clemson, SC 29634, USA
1864 656 7288
Fax: 864 656 4293
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/lab host="TJC121"
/clone lib="Hordeum vulgare
(Fusarium infected)"
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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 5
High quality sequence stop: 668.
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/clone="HVSME10003N10f"
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Hordeum vulgare subsp. vulgare
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(Anote="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plants were grown at the University of Minnesota in the GJ Muchlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 45, 6, and 8 days after Fusarium graminearum incoulation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wingy Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
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                                       Email: rwing@clemson.edu
Total hq bases = 598
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 755.
                                                                                                                                                                                                                                                                                     db xref="taxon:112509"

clone="HVSME10014017f"

tissue_type="Spike"

lab_host="TJC121"
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cultivar="Morex"
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/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhOI; Plants were grown at the University of Minnescra in the GY Muchbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TU Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Akkins and Ming). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or environments.
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http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ. Wing R. Kleinhofs A. Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Neweletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 TCCCGACGACCCAAAAGCCTGTAATTCTATTGCAGCTCAACTTCATCAAGGGGGGACTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           447 CCTCACTGTCAACGGACAGCACGGTGCTATGGATATGGTAGGCCAAGATGCGGTGATCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AAACTGGGCGTTCTTCACATTCAAGCCCAAGGCCCTGTCAAAGCTTAAGGATGCTGTTC
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Matches 481; Conservative
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Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Malysis of a Fusarium sporotrichioides EST database
Unpublished
                                                                                                                                                                                               EST 10-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:5514"
/clone="12f11fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
i 3' end of CDNA cloned into XhoI site of pBluescript"
i 153 c 121 g 107 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 AGCCGAGGGCATTAGCGAGGAAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGACGT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 871 8e-94 gi|4378882|gb|AAD197 (AF127176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 GACCGAGGCATCAGCGAAGGAACACAGGAACTTCCAAAGATCATTCCATATGAGGAGAC 255
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                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
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library Fusarium sporotrichioides cDNA clone 12filfs 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other ESTS: 12f11fs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 ccrrcadescadesccradadesccratarescratescarescresses
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1. .512
/organism="Fusarium sporotrichioides"
                                                                                                                                                                                               mRNA
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High quality sequence stop: 476.
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Fusarium sporotrichioides
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BI191800.1 GI:14665479
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al Similarity 82.2%;
407; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 405 325 4912
Fax: 405 325 7762
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987 AACAGC
                                                    601 ACCAGC
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Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand, M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
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XhoI; S' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"

151 c 122 g 106 t
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/clone="13b10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
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13b10fs.rl Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone l3b10fs 5', mRNA
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                                                                                                                                                                         CAACTICAICAAGGGGGGACTCAICCICACTGICAAGGACAGCACGGIGCIAIGGAIAI 482
                                                                                                                                                                                          Tel: 405 325 4912
Tex: 405 325 74912
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
857 38-92 gi|4378882|gb|AAD197 (AF127176)
trichothecens3-0-acetyltransfer
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                                                  GAGAAAGGCGGGATACCCTATGGCGATGTTTGACGAGAACATCATCGCGCCAAGGAAGAC 362
 256 ACCCGTCTTGTGGTGAAAGACCTCCGTGATGATTCCTCAGGGCCAACGATCGAGGGGTT
                                                                               GAGAAAGGCGGGTTTCCCCTTAGAGATGTTTGACGAGAACGTCGTCGCTCCGAGGAAGAC
                                                                                                               GTTACCTATTGGACCTGGTACTGGTCCCGACGACCAAAGCCTGTAATTCTATTGCAGCT
                                                                                                                               Other ESTS: 13b10fs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Blochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 508;
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High quality sequence stop: 450.
Location/Qualifiers
1.508
/organism="Pusarium sporotrichioides"
/mol type="mRNA"
/strain="Til 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.8%; Pred. No. 7.2e-89; Matches 405; Conservative 0; Mismatches 90;
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Fusarium sporotrichioides
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1 (bases 1 to 498)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioldes EST database
Unpublished
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
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Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
743 8e-79 gi|4378882|gb|AAD197 (AF127176)
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                                                                                                                                                                      CTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAA 182
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                                                           CCAAATCAGICTCCTCTACCCCGTCTCTGATTCCTCTCAAIAICCCACIAITGTCAGCAC
                                                                                      243 Tecregrerrerangacerecesesargarerresesesesesesesargarera
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GTCTTTTGACATAGAGCTCGACATCATCGGCCAG¢AACCGCCTCTTCTTTCAATCTACAC
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/mol_type="mRNA"
/strain="Tri 10"
/bx rref="taxon:5514"
/clone="01e06fs"
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High quality sequence stop: 476.
Location/Qualifiers
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BI200717.1 GI:14666689
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Fax: 405 325 7762
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                                 /note="Vector: pBlueScript SK-; Site 1: EcoR1; Site 2: Xho1; 5' end of cDhA cloned into EcoR1 site of pBluescript; 3' end of cDhA cloned into XhoI site of pBluescript" 156 c 113 g 109 t
/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Bereman, M. and Roe,B.

Analysis of a Fusarium sporotrichioides EST database
Contast: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma

Advanced Center for Genome Technology, University of Oklahoma

G.O Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                          TGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAAAACTATACGATTGGCCCCGAGG
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                                                                                                                                                                                                               TCATCCTCACTGTCAACGGACAGCACGGTGCTATGGATATGGTAGGCCAAGATGCGGTGA
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11f11fs.fl Fusarium sporotrichioides Tri 10 overexpressed CDNA
11brary Fusarium sporotrichioides CDNA clone 11f11fs 3', mRNA
                                                                                                                                                                                3;
                                                                                                                                           Score 323.4; DB 12; Length 498;
Pred. No. 5.2e-81;
); Mismatches 101; Indels 3;
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Fax: 405 325 7762
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/mote="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: Xbol; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript" a 135 c 119 g 131 t
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Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
is the best homolog from a blastx search of Genbank nr 04-09-01
se follochecene3-0-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 428.

Location/Qualifiers
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 481)
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80.7%; Pred. No. 2.4e-79;
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TITLE JOURNAL COMMENT

FEATURES

AUTHORS

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Location/Qualifiers
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/mol_type="mRNA"
/strain="Tri 10"
/db xref="taxon:5514"
/clone="13b10fs"
/clone lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
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XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"
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Contact Dr. Marian Beremand regarding clone availability Included
Contact Dr. Marian Beremand regarding clone availability Included
Tas the best homolog from a blastx search of Genbank nr 04-09-01
745 4e-79 gi|4978882|gb|AAD197 (AF127176)
trichothecene3-0-acetyltransfer
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Analysis of a Fusarium sporotrichioides EST database
Unpublished
Other ESTs: 13b10fs.rl
Other ESTs: 13b10fs.rl
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Pex: 405 325 7762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 296.6; DB 12
Pred. No. 2.2e-73;
0; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: M13-20
High quality sequence stop: 340.
Location/Qualifiers
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Best Local Similarity 80.5%;
Matches 347; Conservative
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1 (bases 1 to 514)
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,M. and Roe,B.
M. and Roe,B.
Unpublished
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/clone=lideOgfs"
/clone=lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"
1 162 c 112 g 105 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294
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Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
Advanced Center for Genome Technology, University of Oklahoma
Advanced Center for Genome Technology, University of Oklahoma
Col Parxington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Fax: 405 325 7762
Fax: 405 325 7762
Fax: 405 325 7762
Fax: 405 325 7762
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
Til 4377882[ab]AAN197 (AF127176)
                                                                                                                                                                                                                               Eukaryota; Fungi, Ascomycota, Pezizohycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 ICCICGIGITGIAGIGAAAGACCICCGCGAIGAICCIICAGCGCCCACGAICGAGGGIAI
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14c09fs.rl Fusarium sporotrichioides Tri 10 overexpressed cDN
library Fusarium sporotrichioides cDNA clone 14c09fs 5', mRNA
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/organism="Fusarium sporotrichioides"
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Pred. No. 3.6e-68;
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1134 TTCTTGGGCCAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGA 1193
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Pred. No. 8.8e-67;
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Best Local Similarity
Matches 322; Conserv
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Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
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cDNA_library"
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                                                                                                 EST 10-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
591 48-61 gi | 4378882 | 91 AAD197 (AF127176)
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Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusarium.
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library Fusarium sporotrichioides cDNA clone b2d04fs 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 GACAGGACGGTGCTATGGATATGGTAGGCCAAGATGCGGTGATCCGTCTACTCTCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GACAACATGGTGTATGGACATGACAGGACAAGATGCAATTATTCGTCTTCTCTCCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 AAGCTGATGTAGCTGGTGACGCTGTTCTCACGCCGGTCAGTGCAAGCTGGGCGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AACC---TGGGCGTGCTGGGGGGGGGGGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             581 CGATAGTTCCTTACCTTGAAAACTATACGATTGGCCCCCGAGGTAGATCATCAGATTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTS: b2d04fs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry University of Oklahoma
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Pax: 405 325 7762
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  514
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ATTAGCTATCGGACCTGGCAATGGCCCCAACGACCGAAG
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                                                                                               411 bp
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Location/Qualifiers
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/strain="Tri 10"
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Best Local Similarity
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Ren, O., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.

Analysis of a Fusarium sporotrichioides EST database
Unpublished
Contact: Burce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912

Fax: 405 325 7762
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/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
694 4e-73 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-0-acetyltransfer
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                                                                         298 TITCALICACICCCAAGGCCCTCTCGGAGCTGAAAGACGCAGCCACAAAGACTCTTGACG
TCACATTCAGCCCCAAGGCCATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI201068 448 bp mRNA linear EST 10-JUL-04612fs.fl Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone 04612fs 3', mRNA
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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Other ESTS: b2d04fs.rl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Partington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
655 5e-70 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-0-acetyltransfer
Seq primer: M13-20
High quality sequence stop: 257.
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                                                                 306 GACCGAGGGCATCAGCGAAGGAAACACAGGAACTTCCAAGATCATTCCATATGAGGAGAC 365
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Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremai, M. and Roe, B. Analysis of a Fusarium sporotrichioides EST database
                                                                                                                   183 AGCCGAGGCATTAGCGAGGAAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGACGT
                                                                                                                                                                                                                      243 TCCTCGTGTTGTAGTGAAAGACCTCCGCGATGATCTTCAGCGCCCCACGATCGAGGGTAT
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b2d04fs.fl Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone b2d04fs 3', mRNA
                       CTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAAGGTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 ATTAGCTATCGGACCTGGCAATGGCCCCAACGA 518
                                                                                                                                                                                                                                                                                                                                                                                                                             363 GITACCTAITGGACCTGGTACTGGTCCCGACGA 395
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/strain="Tri 10"
/db_xref="taxon:5514"
/clone="b2d04fs"
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Fusarium sporotrichioides
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BI187780.1 GI:14661459
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Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Umpublished
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/clone="14b10fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
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14b10fs.rl Fusarium sporotrichioides Tri 10 overexpressed CDNA library Fusarium sporotrichioides CDNA clone 14b10fs 5', mRNA
                                                                              GACTGTGAGACGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCCCAAGAA 1253
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                                                                                                                                149
TICCIGGGCCAAGGIGGGATGCTGGAGTATGACTTTGGGTTTGGACTGGGTAAGCCTGA 209
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Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
712 3e-75 gi|4378882|gb|AAD197 (AF127776)
trichothecene3-0-acetyltransfer
                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                           148 GCCTGATGGGGAGTTTACGGCGTCCATTTCTCTGAGGATGAGGATATGGAGAGAGTAAA
                                                                                                                                208 GAGTGTGAGAAGACCTCGCTTTGAACCTTTTGAGAGTTTTGATGTACTTTATGCCCCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Parrington Oval, Norman, OK 73019, USA 7919, 405 325 4912

Fax: 405 325 7762
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Pred. No. 1.2e-66;
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                                                                                                                                                                                                                                                                                     1314 GGCGGATAAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
                                                                                                                                                                                                                                                                                                                                  88 GGCGGATGAGGAGTGGACAAAGTACGCAAAGTATATTGGGTAG 46
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|mol_type="mRNA"
|strain="Tri 10"
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0; Mismatches
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Location/Qualifiers
1. .518
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Fusarium sporotrichioides
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BI191997.1 GI:14665676
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Best Local Similarity 80.9%;
Matches 318; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
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JOURNAL
COMMENT
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BI191997
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Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 652 3e-68 gi|4378882|gb|AAD197 (AF127176)
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Hypocreomycetidae, Hypocreales, mitosporic Hypocreales, Fusarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCTTACCTTGAAAACTATACGATTGGCCCCGAGGTAGATCATCAGATTGTCAAAGCTG
                                                                                                                                                                                                                                                                                                       347 TCGCGCCAAGGAAGACGTTACCTATTGGACCTGGTACTGGTCCCGACGACCAAAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                   1 rcdcrccaadaadacarradcrarcaaccradcaaradcccccaacaaccaadccrc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 -TGCGCCTGCGGAGCGCTCCACCCGCACGGCCAAGGCAAGCTGGGCGTTCTTTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 ACGGIGCIAIGGAIAIGGIAGGCCAAGAIGCGGIGAICCGICIACICICCAAGGCGIGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647 AIGTAGCIGGIGGIGACGCIGIICICACGCCGGICAGIGCAAGCIGGGCGIICITCITCACAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 TAATICTATIGCAGCICAACTICAICAAGGCGGACTCAICCICACTGICAACGGACAGC
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Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                 Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. (bases 1 to 423) The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state o
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/mol type="mRNA"
/strain="Tri 10"
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                                                                                                                                             Score 258; DB
Pred. No. 2e-67
0; Mismatches
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Seg primer: M13-20
High quality sequence stop: 290.
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80.2%;
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                                                                                                                                                                                                                 Matches 316; Conservative
                     121
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ACTCGACCATCGGCGAAATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTT 1006
                                                                                                                                                         1007 CAGAACTCGACCCCGCGAGCATGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACA 1066
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1 (bases 1 to 392)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1247 CCAAGAAGCCTGATGGCGAGTTCTGTGCGGCGCTTTCTCTGAGGATGAGGATATGGACC 1306
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/clone lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 AGCCTGAGAGTGTGAGAAGACCTCGCTTTGAACCTTTTGAGATTTTGATGTACTTTATGC 156
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Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry Daiversity of Oklahoma
Advanced Center for Genome Technology, University of Oklahoma
620 Parxington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
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High quality sequence stop: 361.
Location/Qualifiers
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EST 10-JUL-2001

Peterson, A., Beremand

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completed: February
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Best Local S
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Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 490)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M. and Roe, B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
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cDNA library"
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Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
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Pred. No. 1.7e-61;
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Best Local Similarity 79.6%;
Matches 301; Conservative
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Fax: 405 325 7762
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/strain="Tri 10"
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XhoI; 5' end of cDNA cloned into EcoR1 site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript"
1 153 c 104 g 103 t 1 others
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High quality sequence stop: 443.
Location/Qualifiers
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Local Similarity 81.1%;
les 292; Conservative
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us-10-614-954-5.rnpb

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7, 2004, 21:46:44; Search time 530 Seconds (without alignments) 9424.540 Million cell updates/sec
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5: / cgn2_6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*
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7: / cgn2_6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Sequence 5, Appli	ì -	; ;	Semience 10 Amel	,	Semience 27681	Segment Controls	Segmence 37751 A	Semience 352 ann	Special Case appropriate	Segmence 24. Appl	Segmence 136. Ann	136	025	Sequence 31187, A	
		ID		US-10-074-279-5	US-10-074-279-1	US-10-074-279-11	US-10-074-279-10	US-10-074-279-7	US-10-369-493-27681	US-10-320-797-7	US-10-369-493-37751	US-10-184-644-352	US-10-184-634-352	US-10-063-685-24	US-10-184-644-136	US~10-184-634-136	US-10-374-780A-932	US-10-027-632-31187	
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ALIGNMENTS

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                                                                                  APPLICANT: Salmeron, J.
APPLICANT: Salmeron, J.
APPLICANT: Selers, C.
APPLICANT: Reinders, D.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Ruznia, R.
APPLICANT: Ruznia, R.
APPLICANT: Ruznia, R.
APPLICANT: Bill-mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/10/074,279
CURRENT FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2000-03-29
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100.0%; Pred. No. 0;
iive 0; Mismatches
                   Sequence 5, Application US/10074279
Publication No. US20020162136Al
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 1356
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Best Local Similarity 100.
Matches 1356; Conservative
US-10-074-279-5
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Publication No. US20020162136A1
GENERAL INFORMATION:
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APPLICANT: Hohn, T.
APPLICANT: Salmeron, J.
APPLICANT: Peters, C.
APPLICANT: Kendra, D.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.

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APPLICANT: Dill-Mackey, R.
TITLE OF INVENTION: Transgenic Plant and Methods;
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/10/074,279
CURRENT FILING DATE: 2002-02-12;
PRIOR APPLICATION NUMBER: US/09/538,414
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                  Score 915.6; DB 14;
Pred. No. 4.7e-306;
0; Mismatches 264;
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Best Local Similarity 80.3%;
Matches 1087; Conservative
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; ORGANISM: Plasmid
US-10-074-279-11
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                                                                                                                                   AATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCGACCCGC
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                                          CGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTTGATGCTCGACCGGCAATGGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10. Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Balmeron, J.
; APPLICANT: Reidra, C.
; APPLICANT: Reidra, J.
; APPLICANT: Reidra, J.
; APPLICANT: Reidra, J.
; APPLICANT: Reidra, S.
; APPLICANT: Reidra, S.
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; APPLICANT: Reidra, S.
; APPLICANT: Reidra, S.
; APPLICANT: Reidra, S.
; APPLICANT: Right, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; TILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT APPLICATION NUMBER: US/09/538,414
; RIGN FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE PATENTIN Ver. 2.0
; SEQ ID NO 10;
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Best Local Similarity 80.3%;
Matches 1087; Conservative
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ORGANISM: Plasmid
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                                                                                                                                               CAAGATGCGGTGTCTCCTCTCCAAGGCGTGCCGTAACGACCCATTCACCGAAGAG
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                                                            ATCAAGGGCGGACTCATCCTCACTGTCAACGGACAGCACGGTGCTATGGATATGGTAGGC
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                                                                                                                                                                                                                                                                      510 ATT---GGCCCCGAGGIAGAICAICAGAITGICAAAGCIGAIGIGAGCIGGIGGIGACGCI
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Publication No. US20030233675A1
GENERAL INFORMATION:
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Pred. No. 2.4e-75;
0; Mismatches 622; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kuznia, R.
APPLICANT: Kuznia, R.
TITLE OF INVENTION Transgenic Plant and Methods
TITLE OF INVENTION Transgenic Plant and Methods
FILE REFERENCE: Sequencelist
CURRENT APPLICATION NUMBER: US/10/074,279
CURRENT FILING DATE: 2002-02-12
PRIOR PLING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO.
SEQ ID NO.
                                                                                                                                                                                                                                                                                            GGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
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Publication No. US20020162136A1
GENERAL INFORMATION:
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APPLICANT: Salmeron, J.
APPLICANT: Peters, C.
APPLICANT: Kendra, D.
APPLICANT: Keinders, J.
APPLICANT: Keinders, J.
                                                                                                                                                                                                                                                                                                                                                                                           US-10-074-279-7
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXAMES WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 37751
LENGTH: 2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1375 GECCTGETCGCCTGGACCTGGCGACCGGCAAGGTGCGCTGGAACTACCAGTTCACCCAC 1434
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NUMBER OF SEQ ID NOS: 612
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Pred. No. 0.
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                                                                                                                             ; Sequence 37751, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.4%;
Matches 66; Conservative
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Gurney, Austin L
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Watanabe, Colin
Wood, William I.
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US-10-184-644-352
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LENGTH: 837
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APPLICANT:
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APPLICANT:
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Best Local
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APPLICANT: Enciliant Carlos
APPLICANT: Zamudio, Carlos
TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 10182-021-999
CURRENT APPLICATION NUMBER: US/10/320,797
CURRENT APPLICATION NUMBER: 60/341,261
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 3361
SOFTWARE: Patentin version 3.1
                                                                             APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27681
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Pred. No. 0.038;
0; Mismatches 73;
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Publication No. US20040014955A1
GENERAL INFORMATION:
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Cao, Yongwei
Hinkle, Gregory J.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Neurospora crassa
US-10-369-493-27681
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Best Local Similarity 53.2%
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Matches 76; Conserv
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1135 TCTTGGGCCAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCGAG 1194
          1015 GACCCCGCGAGCATGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACAACCCC 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 ..NNC.NT.CNCABT..RYSMCMCNWGHH.NCNCTTKY.HNGBNS..SSW.MMT.M.M.M.390
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                                APPLICANT: Watanabe,Colin K.
APPLICANT: Wood,William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,685
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 24
LENGTH: 556
                                                                                    1075 GACAAGTCCAACGTATCCCTGACGCTGATGCGGACCCATCTACCAGCGTCATGCTGAGT
                                                                                                            ..b..T..MH..GDCRCNH..HA..YTSG.SW....HBDTKB.TKBDYSAS..CN.S.G.
                                                                                                                                                                                    825 CGTGCGTCTCGAAGAATCGATGGCTCTGCACCTACCGAGTTCTGCCGTGCTGTTGATGC
                                                                                                                                                                                                                                        1195 ACTGTGAGACGCCAATCTTTGAGCCTGTTGAGAGCTTGATGTACTTTATGCCC 1248
                                                                                                                                                                                                                                                                  , DB 13; Length 556;
0.56;
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1 Similarity 7.4%; Pred. No. 0.56;
33; Conservative 142; Mismatches 268; Indels
                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 24, Application US/10063685; Publication No. US20030180909A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
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APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                      495 G.ACHTW.SDMA.GKTDCN.DCSGW.TTG......GDYSH.C.A.G.YHTRHRMC..AB
                                                          895 ATGGGTGTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACC
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P943-0816.217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 352, Application US/10184634 Publication No. US20030068684A1 GENERAL INFORMATION:
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Wood, William I.
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Goddard, Audrey
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Best Local Similarity
Matches 52; Conserv
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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                                                                              APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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                         US-10-184-634-136/c
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Best Local S
Matches 33
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ORGANISM:
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Pred. No. 0.56;
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NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
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                                         945 CAACTCGACCATCGGCGAAATCG 967
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                                                                                                                                      Sequence 136, Application US/10184644 Publication No. US20030044930A1 GENERAL INFORMATION:
                                                           SBBSM.HHMS..SRM..K..SG
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Best Local Similarity 7.4%; Pred
Matches 33; Conservative 142;
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Gurney, Austin L.
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Smith, Victoria
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Goddard, Audrey
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ORGANISM: Homo Sapien
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149 RYM..B..HM.
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509 S.G. R.GCSCSC.CSS.HS.H..HBHNCNRTNMKWSAKBY.TK..Y...H.MSAHB.B 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    525 CCGTAACGACCCATTCACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGAT 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 ..NNC.NT.CNCABT..RYSMCMCNWGHH.NCNCTTKY.HNGBNS..SSW.NMT.M.M.M. 390
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                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430RTC217 CURRENT APPLICATION NUMBER: US/10/184,634 CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATGTAGCTGGTGGTGACGCTGTTCTCACGCCGGTCAGTGCAAGCTGGGCGTTCTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             765 AACAAAGTICGIGICGACIGACGAIGCICTTICGGCGIICAICIGGAAAICGGCCICICG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7.4%; Pred. No. 0.56; Congth 55 Similarity 7.4%; Pred. No. 0.56; Conservative 142; Mismatches 268; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            945 CAACTCGACCATCGGCGAAATCG 967
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US-10-374-780A-932
; Sequence 932, Application US/10374780A
; Publication No. US20040019927A1
; PRDMICALION SPERMAL INFORMATION:
; APPLICANT: Sherman, Bradley K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
Sequence 136, Application US/10184634
Publication No. US20030068684A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GCTACTGCTACCACCAAATATATAAATCTATATATTTCATTTCCCTTCGCCCTTCAGAA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G568 US-10-374-780A-932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AAAAAATGCACACGACAAGACCAACAACATATTCCTTCTCGATCTTAACTTTGTACT
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                       APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell III, Arnold T
APPLICANT: Pineda, Omaira
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
TITLE REPERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374, 780A
PRIOR APPLICATION NUMBER: 09/837, 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.6%; Score 34.6; DB 12; Length 427; ilarity 50.3%; Pred. No. 0.67; Conservative 0; Mismatch...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR PILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 932
LENGTH: 427
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Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-04-18
APPLICATION NUMBER: 60/310,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR PLILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR PLILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR PELING DATE: 2001-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
echmann, Jose Luis
ang, Cai-Zhong
ard, Jacqueline E
                                                                                               Creelman, Robert A
                                                                                                                                                                         teuber, T. Lynne
                                                                                                                                                                                                                        Broun, Pierre E
                                                                                                                                                                                                   James
                                                                                                                                                  Adam, Luc J
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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                              Keddie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Zea mays FEATURE;
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US-10-027-632-31187
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.001 TTCGTTCAGAACTCGACCCCGCGAGCATGCGCCCAGCGAACAAGAGGTCTCGCGACGTACC 1060
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Pred. No. 1.1;
0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1061 IGCACAACAACCCCGACAAGTCCAACGTATCCC 1093
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                                           PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-00
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 2000-00-29
PRIOR FILING DATE: 1090-11-23
PRIOR PPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 31187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 7, 2004, 23:31:24
Job time : 532 secs
                              PRIOR APPLICATION NUMBER: US 60/218,006
2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.6%;
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Best Local Similarity 51.6
Matches 79; Conservative
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

7, 2004, 20:53:23 February Run on:

; Search time 94 Seconds (without alignments) 6367.186 Million cell updates/sec

US-10-614~954-5 1356

1 atggctttcaagatacagct.....atgcgcagtacgttggttag 1356 Perfect score: Sequence:

IDENTITY NUC Scoring table:

569978 seqs, 220691566 residues Gapop 10.0 , Gapext 1.0 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/packfiles1.seq:* Issued Patents NA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			οķe			SUMMARIES	
Result No.	ult No.	Score	Query Match	Length	DB	ID	Description
	1	1356	100.0	1356	4	US-09-538-414-5	Sequence 5. Appli
	Ŋ	915.6	67.5	1403	4	-414	-
	m	915.6	67.5	12949	4	538-414	7
	4	915.6	67.5	13737	4	538	10
	Ŋ	249.8	18.4	1425	4	US-09-538-414-7	
	9	39.8	2.9	4403765	æ	US-09-103-840A-2	2 .
	7	39.8	2.9	4411529	٣	US-09-103-840A-1	i -
	æ	34.2	2.5	720	4	US-09-252-991A-16032	٤
υ	σ	34.2	2.5	1074	4	US-09-252-991A-16568	16568.
	10	34.2	2.5	2721	4	US-09-252-991A-16144	16144
υ	11	33.4	2.5	516	4	US-09-252-991A-15293	15293
	12	33.4	2.5	1614	4	US-09-252-991A-15438	1543
U	13	32.8	2.4	1230025	4		1
	14	32.4	2.4	1620	4	US-09-125-642C-9	σ
	15	32.4	2.4	1740	4	US-09-125-642C-2	
	16	32.4	2.4	1742	4	US-09-125-642C-13	, ~
	11	32.4	2.4	5515	4	US-09-125-642C-8	ω,
	18	32.4	2.4	5519	4	US-09-125-642C-12	12
บ	19	32.2	2.4	1482	4	US-09-252-991A-8923	8923
	20	32.2	2.4	1782	4	US-09-252-991A-9072	
	21	32.2	2.4	2121	4	US-09-252-991A-9159	9159,
บ	22	m	2.4	1406	4	US-09-699-266A-10	10, A
	23	31.4	2.3	1482	4	US-09-252-991A-1338	1338
บ	24	31.4	2.3	1671	4	US-09-252-991A-1222	1222,
	25	Η.	2.3	1917	4	US-09-252-991A-1386	1386,
	56	31.4	2.3	2190	7	US-08-492-027A-7	7, App
	27	31.2	2.3	456	4	US-09-252-991A-6665	99

Sequence 64, Appl	Seguence 6694. Ap			Sequence 3, Appli	-	3,	m	7	ω,	Sequence 3, Appli	<u>ر</u>	7	Sequence 9985, Ap				•
US-09-410-551B-64	US-09-252-991A-6694	US-09-252-991A-6607	US-09-410-551B-20	US-09-691-861A-3	US-09-410-551B-1	US-08-459-568-3	US-08-399-411-3	US-08-605-106-7	US-08-516-859A-3	US-09-586-472-3	US-09-528-706-3	US-09-252-991A-10039	US-09-252-991A-9985	US-09-252-991A-9806	US-09-410-551B-68	US-09-252-991A-7942	US-09-252-991A-7538
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2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.5	2.2	2.2
31.2	31.2	31.2	31.2	31.2	31.2	31	31	31	31	31	31	30.6	30.6	30.6	30.4	30.4	30.4
28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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61 ACCCAAATCAGTCTCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTCAGC 120
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ACCULT 1
US-09-518-414-5
Sequence 5, Application US/09538414
Sequence 5, Application US/09538414
Setent No. 6346655
GENERAL INFORMATION:
APPLICANT: Hohn, T.
APPLICANT: Salmeron, J.
APPLICANT: Reinders, C.
APPLICANT: Kendra, D.
APPLICANT: Kendra, D.
APPLICANT: Kendra, D.
APPLICANT: Koraina, R.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFERENCE: Sequencelist
CURRENT APPLICATION NUMBER: US/09/538,414
CURRENT FILING DATE: 2000-03-29
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1356; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-09-538-414-5
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Best Local Similarity 100.
Matches 1356; Conservative
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APPLICANT: Salmeron, J.
APPLICANT: Rendra, D.
APPLICANT: Rendra, D.
APPLICANT: Rendra, D.
APPLICANT: Rendra, D.
APPLICANT: Reinders, J.
APPLICANT: Rinia, R.
APPLICANT: Numia, R.
TITLE OF INVENTION: Transgenic Plant and Met
FILE REPERBNCE: sequencelist
CURRENT APPLICATION NUMBER: US/09/538,414
CURRENT FILING DATE: 2000-03-29
SOFTWARE: Patentin Ver. 2.0 ORGANISM: Fusarium sporotrichioides 663 693 à

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                        11641 ATTAGCTATCGGACCTGGCAATGGCCCCCAACGACCCGAAGCCTGTGTTGCTATTGCAGCT
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                                                                                                        11341 CCAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCCAGTATCCCACCATCGTCAGCAC
                                                                                                                                          CTTCGAGCAAGGTCTTAAGCGCTTCTCCGAAGCCGTCCCATGGGTCGCAGGCCAGGTCAA
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GGCTTTCAAGATACAGCTCGACACCCTCGGCCAGCTACCAGGCCTCCTTTCGATCTACAC
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1142 1186 1306 1066 AATCGCCAACGAGTCACTCGGCGCAACAGCATCACGCCTTCGTTCAGAACTCGACCCCGC 1022 cecrececedeacedagedagengedentringaricalicadedageden 766 GICAGAGCICAAGGAIGCIGCIACCAAGACICTIGACGCAICAACAAAGTICGIGICGAC 782 826 482 602 947 ATCAAGCACATACCCAGGCCTTCTTCAAACATGACCTACCATGACTCGACCGTCGCCGA 1007 AATCGCCAACGAACCACTTGGCGCAACAGCATCACGCCTGCGCTCGGAACTCAACAGG a de la contra dela contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra dela contra de la contra de la contra de la contra de la contra de la contra de la contra dela contra de la contra del la contra CGAGITCTGTGCGGCGCTTTCTCTGAGGGATGAGGATATGGACCGATTGAAGGCGGATAA CGAAGAGGAAATGACGCCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAAAA crceeaecreaaaeacecaecacaaaaaacrcrreacecececaacrreaac rgargargcrichtrogogittratorogoaricacotocogogiacorocosagari CGATGGCTCTGCACCTACCGAGTTCTGCCGTGTTGATGCTCGACCGGCAATGGGTGT 887 géargerrecacaceracraarrergecececrererecagacargedegececaargegeer CICGAACAACIACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACCATCGGCGA GAGCATGCGCCAGCGAACAAGAGGTCTCGCGACGTACCTGCACAACAACAACCAAGTC 1083 CAACGTATCCCTGACGCTGATGCGGACCCATCTACCAGCGTCATGCTGAGTTCTTGGGC gaggercrecergacegeceargegaarecercaageageareargagreerggge CAAGGTGGGACTCTGGGATTACGACTTTGGGCTCGGACTGGGTAAGCCCCGAGACTGTGAG 1187 caaggroccarccroccagrarcacriricccririccacrocccraacccrocagagges ACGGCCAATCTTTGAGCCTTGAGAGCTTGATGTACTTTATGCCCAAGAAGCCTGATGG 410 ATTAGCTATCGGACCTGGCATGCCCCAACGACCCAAGCCTGTGTTGCTATTGCAGCT CAACTICATTAAGGGGGGACTCATTCTCACCGTGAACGGACAACATGGTGCTATGGACAT CGCTGTTCTCACGCCCGGTCAGGTGCTGGGCGTTCTTCACATTCAGCCCCAAGGCCAT CAACTTCATCAAGGGGGGACTCATCCTCACTGTCAACGGACAGGCACGGTGCTATGGATAT GGTAGGCCAAGATGCGGTGATCCGTCTCTCCAAGGCGTGCCGTAACGACCCATTCAC CTATACGATTGGCCCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGGTGA 363 GTTACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGCCTGTAATTCTATTGCAGCT

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Pred. No. 1.5e-69;
0; Mismatches 622; Indels 27;
                             GENERAL INC. 5346555

GENERAL INCORMATION:
APPLICANT: Hohn, T.
APPLICANT: Peters, C.
APPLICANT: Reinders, D.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
APPLICANT: Reinders, J.
TITLE OF INVENTION: Transgenic Plant and Methods
FILE REFREENCE: sequencelist
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Saccharomyces cerevisiae
Application US/09538414
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51.9%;
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Matches 700; Conservative
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718 GCCATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGCATCAACAAAGTTCGTG
                                       781 TCATTGCAGAATCTGAGGATTTTGGCAGATGCAGACATGTACTTCTGGCACAAAATTTGTC
                                                                                            841 TCCACTGATGATACGTCACTGCTTTCATCTGGAAATCAGTTTCTCGAGCCGGTTATCT
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                                                                                                                                                                                                                                                                                    898 GGTGTCTCGAACAACTACCCAGGCCTTCTTCAAAACATGACCTACCACAACTCGACCATC
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FASSER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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OTHER INFORMATION: "n" bases at various positions throughout
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ORGANISM: Mycobacterium tuberculosis
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Length 4403765;

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Query Match

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Sequence 16144, Application US/09252991A Patent No. 6551795
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US-09-252-991A-16144
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LENGTH: 1074
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Patent No. 6551795;
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
FILE REFERENCE: 107196.136
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Pred. No. 1.3;
0; Mismatches 102;
Pred. No. 1.3;
0; Mismatches 102;
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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CTHER INFORMATION: H37Rv
US-09-103-840A-1
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
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APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
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Matches 101; C
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PARENEAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVERNION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: 08/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                          Score 34.2; DB Pred. No. 0.74;
; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 16032
                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 53.3%;
Matches 72; Conservative
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Best Local Similarity
Matches 72; Conserva
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GENERAL INFORMATION:
APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
                                                                 Sequence 15438, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 2.1;
0; Mismatches 66; Indels 0;
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CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION WUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15438
LENGTH: 1614
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature
LOCATION: (45001)...(60000)
OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature
LOCATION: (60001)...(75000)
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ORGANISM: Pseudomonas aeruginosa
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NUMBER OF SEQ ID NOS: 6849
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LOCATION: (15001)..(30000)
OTHER INFORMATION: ni=a or c or
NAME/KEY: misc_feature
LOCATION: (30001)..(45000)
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Best Local Similarity 52.5%;
Matches 73; Conservative
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OTHER INFORMATION: n=a or c
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LENGTH: 1230025
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US-09-198-452A-1/c
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     APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 10196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16144
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MOUENTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15293
LENGTH: 516
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; Sequence 15293, Application US/09252991A
; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Thes 72; Conserve
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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990 AGCATCACGCCTTCGTTCAGAACTCGACCCCGCGAGCATGCGCCCAGCGAACAAGAGGTCT 1049
                                                                                                                                                                                                                                                                                                                                    930 AAACATGACCTACCACAACTCGACCATCGGCGAAATCGCCAACGAGTCACTCGGCGCAAC 989
                                                                                                                                                                                                                                                                                                                                                                                72 TAGGIAGITGITGCCCACCICCATGATCCTCGCACGCGCGCGGCGACGCTCGCACGCC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 CGCGGCGGCCGCCGCCGCCGCCGAGGACGGCAAGAACAGTGGCCCGGAAGCGCAAGCG 191
                                                                                                                                                                                                                                                                                     870 CCGIGCTGITGAIGCICGACCGGCAAIGGGIGICICGGAACAACIACCCAGGCCIICIICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09125642C
Patent No. 6365333
GENERAL INFORMATION
APPLICANT: BAYER AG
TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, a
TITLE OF INVENTION: Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Pennsylvania
COUNTAY: U.S.A.
ZIP: 15205-9741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,642C
FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                         0;
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                                                                                                                                             Length 1620;
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                                                                                                                                          Query Match 2.4%; Score 32.4; DB 4; Length 1 Best Local Similarity 46.8%; Pred. No. 4.3; Matches 102; Conservative 0; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4%; Score 32.4; DB 4; Length 1 llarity 46.8%; Pred. No. 4.5; Conservative 0; Mismatches 116; Indels
                        ORGANISM: Parapox ovis
STRAIN: D1701 Proteinkinase-Gen F10L (Version2)
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1050 CGCGACGTACCTGCACAACAACCCCGACAAGTCCAACG 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Parapox ovis
STRAIN: D1701- Proteinkinase-Gen(Version 1)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 caagacgcccaacrgcgaagacgccgacaacrccgacg 229
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FILING DATE: 17-Feb-97
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Bayer Corporation
STREET: 100 Bayer Road
CITY: Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 18
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  ORIGINAL SOURCE:
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Best Local Similarity
Matches 102; Conserv
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US-09-125-642C-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, a
Their Production and Their Use in Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1230025,
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           772004 CIGITACIGICGIGGGIGGAGAGAIGCGGCA 771973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 CGCCCACGATCGAGGGTATGAGAAAGGCGGGA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/125,642C
FILING DATE: 20-Aug-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/00729,
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 100 Bayer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (855001)..(870000)
OTHER INFORMATION: n=a or c or g or
                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or
INFORMATION: n=a or c or g or
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LENGTH: 1620 base pairs
                 NAME/KEY: misc_feature
LOCATION: (81001).. (825000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (82501).. (840000)
OTHER INFORMATION: n=a or c or g
LOCATION: (840001).. (855000)
OTHER INFORMATION: n=a or c or g
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 15205-9741
COMPUTER READABLE FORM:
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Best Local Similarity 59.8'
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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US-09-125-642C-9
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Gaps

	192 CAAGACGCCCAACAAGACGCCGAAAATTCGGAG 229	qq
	1050 CGCGACGTACCTGCACAACCCCGACAAGTCCAACG 1087	Qy
	132 CGCGGCGGCGGCGGCCGAGGACGCAAGAACAGTGATCGCCGGAAGCGCAAGCG 191	OP
	990 AGCATCACGCCTTCGTTCAGAACTCGACCCCGCGAGCATGCGCCAGCGAACAAGAGGGTCT 1049	ò
	72 TAGGTAGTTGTTGCCCACCTCCATGATCCTCGCACGCAGGCGGGGGGGG	qa
٠	930 AAACATGACCTACCACAACTCGACGAAAATCGCCAACGAGTCACTCGGCGCAAC 989	δγ
	12 CCATCCCGTTGCTGCGCGACTGCCCTCTGTTTTTTTTTCTTTC	QD
	870 CCGTGCTGTTGATGCTCGACCGGCAATGGGTGTCTCGAACAACAACTACCCAGGCCTTCTTCA 929	ò

Search completed: February 7, 2004, 23:22:31 Job time : 104 secs